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A METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA LIBRARY. APPLICATION TO THE DETECTION OF MYCOBACTERIA.

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I. Background of the invention

[001] The present invention pertains to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given [mycobacterium] ^{mycobacterium} strain, said DNA library being cloned in a bacterial artificial chromosome (BAC). The invention concerns also polynucleotides identified by the above method, as well as detection methods for mycobacteria, particularly *Mycobacterium tuberculosis*, and kits using said polynucleotides as primers or probes. Finally, the invention deals with BAC-based mycobacterium DNA libraries used in the method according to the invention and particularly BAC-based *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG DNA libraries.

[002] Radical measures are required to prevent the grim predictions of the World Health Organisation for the evolution of the global tuberculosis epidemic in the next century becoming a tragic reality. The powerful combination of genomics and bioinformatics is providing a wealth of information about the etiologic agent, *Mycobacterium tuberculosis*, that will facilitate the conception and development of new therapies. The start point for genome sequencing was the integrated map of the 4.4 Mb circular chromosome of the widely-used, virulent reference strain, *M. tuberculosis* H37Rv and appropriate cosmids were subjected to systematic shotgun sequence analysis at the Sanger Centre.

[003] Cosmid clones (Balasubramanian et al., 1996; Pavelka et al., 1996) have played a crucial role in the *M. tuberculosis* H37Rv genome sequencing project. However, problems such as under-representation of certain regions of the chromosome, unstable inserts and the relatively small insert size complicated the production of a comprehensive set of canonical cosmids representing the entire genome.

II. Summary of the invention

[004] In order to avoid the numerous technical constraints encountered in the state of the art, as described hereabove, when using genomic mycobacterial DNA libraries constructed in cosmid clones, the inventors have attempted to realize
5 genomic mycobacterial DNA libraries in an alternative type of vectors, namely Bacterial Artificial Chromosome (BAC) vectors.

[005] The success of this approach depended on whether the resulting BAC clones could maintain large mycobacterial DNA inserts. There are various reports describing the successful construction of a BAC library for eucaryotic organisms
10 (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997) where inserts up to 725 kb (Zimmer et al., 1997) were cloned and stably maintained in the *E. coli* host strain.

[006] Here, it is shown that, surprisingly, the BAC system can also be used for mycobacterial DNA, as 70% of the clones contained inserts in the size of 25 to
15 104 kb.

[007] This is the first time that bacterial, and specifically mycobacterial, DNA is cloned in such BAC vectors.

[008] In an attempt to obtain complete coverage of the genome with a minimal overlapping set of clones, a Bacterial Artificial Chromosome (BAC) library of *M. tuberculosis* was constructed, using the vector pBeloBAC11 (Kim et al., 1996) which combines a simple phenotypic screen for recombinant clones with the stable propagation of large inserts (Shizuya et al., 1992). The BAC cloning system is based on the *E. coli* F-factor, whose replication is strictly controlled and thus ensures stable maintenance of large constructs (Willets et al., 1987).
20 BACs have been widely used for cloning of DNA from various eucaryotic species (Cai et al., 1995; Kim et al., 1996; Misumi et al., 1997; Woo et al., 1994; Zimmer et al., 1997). In contrast, to our knowledge this report describes the first attempt to use the BAC system for cloning bacterial DNA.

[009] A central advantage of the BAC cloning system over cosmid vectors used
30 in prior art is that the F-plasmid is present in only one or a maximum of two copies per cell, reducing the potential for recombination between DNA fragments and, more importantly, avoiding the lethal overexpression of cloned bacterial genes. However, the presence of the BAC as just a single copy means that plasmid DNA has to be extracted from a large volume of culture to obtain

sufficient DNA for sequencing and it is described here in the examples a simplified protocol to achieve this.

[010] Further, the stability and fidelity of maintenance of the clones in the BAC library represent ideal characteristics for the identification of genomic differences possibly responsible for phenotypic variations in different mycobacterial species.

[011] As it will be shown herein, BACs can be allied with conventional hybridization techniques for refined analyses of genomes and transcriptional activity from different mycobacterial species.

[012] Having established a reliable procedure to screen for genomic polymorphisms, it is now possible to conduct these comparisons on a more systematic basis than in prior art using representative BACs throughout the chromosome and genomic DNA from a variety of mycobacterial species.

[013] As another approach to display genomic polymorphisms, the inventors have also started to use selected H37Rv BACs for "molecular combing" experiments in combination with fluorescent *in situ* hybridization (Bensimon et al., 1994; Michalet et al., 1997). With such techniques the one skilled in the art is enabled to explore the genome of mycobacteria in general and of *M. tuberculosis* in particular for further polymorphic regions.

[014] The availability of BAC-based genomic mycobacterial DNA libraries constructed by the inventors have allowed them to design methods and means both useful to identify genomic regions of interest of pathogenic mycobacteria, such as *Mycobacterium tuberculosis*, that have no counterpart in the corresponding non-pathogenic strains, such as *Mycobacterium bovis* BCG, and useful to detect the presence of polynucleotides belonging to a specific mycobacterium strain in a biological sample.

[015] By a biological sample according to the present invention, it is notably intended a biological fluid, such as plasma, blood, urine or saliva, or a tissue, such as a biopsy.

[016] Thus, a first object of the invention consists of a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC).

[017] The invention is also directed to a polynucleotide of interest that has been isolated according to the above method and in [partoular] ^{particular} a polynucleotide containing one or several Open Reading Frames (ORFs), for example ORFs encoding either a polypeptide involved in the pathogenicity of a mycobacterium strain or ORFs encoding Polymorphic Glycine Rich Sequences (PGRS).

[018] Such polynucleotides of interest may serve as probes or primers in order to detect the presence of a specific mycobacterium strain in a biological sample or to detect the expression of specific genes in a particular mycobacterial strain of interest.

[019] The BAC-based genomic mycobacterial DNA libraries generated by the present inventors are also part of the invention, as well as each of the recombinant BAC clones and the DNA insert contained in each of said recombinant BAC clones.

[020] The invention also pertains to methods and kits for detecting a specific mycobacterium in a biological sample using either at least one recombinant BAC clone or at least one polynucleotide according to the invention, as well as to methods and kits to detect the expression of one or several specific genes of a given mycobacterial strain present in a biological sample.

III. Brief description of the Figures.

[021] In order to better understand the present invention, reference will be made to the appended figures which depicted specific embodiments to which the present invention is in no case limited in scope with.

[022] Figures 1A and 1B : PCR-screening for unique BAC clones with specific primers for 2 selected genomic regions of the H37Rv chromosome, using 21 pools representating 2016 BACs (Figure 1A) and sets of 20 subpools from selected positive pools (Figure 1B).

[023] Figure 2 : Pulsed-field gel electrophoresis gel of *Dra*I- cleaved BAC clones used for estimating the insert sizes of BACs.

[024] Figure 3 : Minimal overlapping BAC map of *M. tuberculosis* H37Rv superimposed on the integrated physical and genetic map established by Philipp et al. (18). Y- and I- numbers show pYUB328 (2) and pYUB412 (16) cosmids which were shotgun sequenced during the H37Rv genome sequencing project. Y-cosmids marked with * were shown in the integrated physical and genetic map

(18). Rv numbers show the position of representative BAC clones relative to sequenced Y- and I- clones. Squared Rv numbers show BACs which were shotgun sequenced at the Sanger Centre.

[025] Figures 4A and 4B : Ethidium bromide stained gel (Figure 4A) and
5 corresponding Southern blot (Figure 4B) of *Eco*RI and *Pvu*II digested Rv58 DNA hybridized with ³²P labeled genomic DNA preparations from *M. tuberculosis* H37Rv, *M. bovis* ATCC 19210 and *M. bovis* BCG Pasteur.

[026] Figure 5 : Organisation of the ORFs in the 12.7 kb genomic region present in *M. tuberculosis* H37Rv but not present in *M. bovis* ATCC 19210 and *M. bovis* BCG
10 Pasteur. Arrows show the direction of transcription of the putative genes. Positions of *Eco*RI and *Pvu*II restriction sites are shown. Vertical dashes represent stop codons. The 11 ORFs correspond to the ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library. The junction sequences flanking the polymorphic region are shown.

15 [027] Figure 6 : Variation in the C-terminal part of a PE-PGRS open reading frame in *M. tuberculosis* strain H37Rv relative to *M. bovis* BCG strain Pasteur.

[028] The numbers on the right side of the Figure denote the position of the end nucleotides, taking as the reference the *M. tuberculosis* genome.

[029] Figure 7 : Polynucleotide sequence next to the *Hind*III cloning site in the BAC
20 vector pBeloBAC11 (Kim et al., 1996) used to clone the inserts of the BAC-based myobacterial genomic DNA library according to the invention.

[030] *Not*I : location of the *Not*I restriction sites.

[031] Primer T7-BAC1 : nucleotide region recognized by the T7-BAC1 primer shown in Table 1.

25 [032] T7 promoter : location of the T7 promoter region on the pBeloBac11 vector.

[033] Primer T7-Belo2 : nucleotide region recognized by the T7-Belo2 primer shown in Table 1.

[034] *Hind* III : the *Hind*III cloning site used to clone the genomic inserts in the pBeloBAC11 vector.

30 [035] SP6-Mid primer : nucleotide region recognized by the SP6 Mid primer shown in Table 1.

[037] SP6-BAC1 primer : nucleotide region recognized by the SP6 BAC1 primer shown in Table 1.

SP6 promoter : location of the SP6 promoter region on the pBeloBac11 vector.

IV. Detailed description of the preferred embodiments.

- [038] As already mentioned hereinbefore, the present invention is directed to a method for isolating a polynucleotide of interest that is present in the genome of a mycobacterium strain and/or is expressed by said mycobacterium strain and that is absent or altered in the genome of a different mycobacterium strain and/or is not expressed in said different mycobacterium strain, said method comprising the use of at least one clone belonging to a genomic DNA library of a given mycobacterium strain, said DNA library being cloned in a bacterial artificial chromosome (BAC) type vector.
- 10 [039] For this purpose, the inventors have constructed several BAC-based mycobacterial genomic DNA libraries that may be used in order to perform the above described method.
- [040] Because it is the first time that mycobacterial genomic DNA has been successfully cloned in BAC type vectors, and because these DNA libraries are then novel and nonobvious, an object of the present invention consists in a mycobacterial genomic DNA library cloned in such a BAC type vector.
- 15 [041] As an illustrative example, a BAC-based DNA library of *Mycobacterium tuberculosis* has been realized. Forty-seven cosmids chosen from the integrated map of the 4.4 Mb circular chromosome (Philipp et al., 1996a) were shotgun-sequenced during the initial phase of the H37Rv genome sequence project. The sequences of these clones were used as landmarks in the construction of a minimally overlapping BAC map. Comparison of the sequence data from the termini of 420 BAC clones allowed us to establish a minimal overlapping BAC map and to fill in the existing gaps between the sequence of cosmids. As well as using the BAC library for genomic mapping and sequencing, we also tested the system in comparative genomic experiments in order to uncover differences between two closely related mycobacterial species. As shown in a previous study (Philipp et al., 1996b), *M. tuberculosis*, *M. bovis* and *M. bovis* BCG, specifically BCG Pasteur strain, exhibit a high level of global genomic conservation, but certain polymorphic regions were also detected. Therefore, it was of great interest to find a reliable, easy and rapid way to exactly localize polymorphic regions in mycobacterial genomes using selected BAC clones. This approach was validated by determining the exact size and location of the polymorphisms in the genomic region of *DraI* fragment Z4 (Philipp et al., 1996b), taking advantage of the availability of an appropriate BAC clone covering the polymorphic region and
- 20
- 25
- 30
- 35

the H37Rv genome sequence data. This region is located approximately 1.7 Mb from the origin of replication.

[042] The Bacterial Artificial Chromosome (BAC) cloning system is capable of stably propagating large, complex DNA inserts in *Escherichia coli*. As part of the
5 *Mycobacterium tuberculosis* H37Rv genome sequencing project, a BAC library was constructed in the pBeloBAC11 vector and used for genome mapping, confirmation of sequence assembly, and sequencing. The library contains about 5000 BAC clones, with inserts ranging in size from 25 to 104 kb, representing theoretically a 70 fold coverage of the *M. tuberculosis* genome (4.4 Mb). A total
10 of 840 sequences from the T7 and SP6 termini of 420 BACs were determined and compared to those of a partial genomic database. These sequences showed excellent correlation between the estimated sizes and positions of the BAC clones and the sizes and positions of previously sequenced cosmids and the resulting contigs. Many BAC clones represent linking clones between sequenced cosmids,
15 allowing full coverage of the H37Rv chromosome, and they are now being shotgun-sequenced in the framework of the H37Rv sequencing project. Also, no chimeric, deleted or rearranged BAC clones were detected, which was of major importance for the correct mapping and assembly of the H37Rv sequence. The minimal overlapping set contains 68 unique BAC clones and spans the whole
20 H37Rv chromosome with the exception of a single gap of ~ 150 kb. As a post-genomic application, the canonical BAC set was used in a comparative study to reveal chromosomal polymorphisms between *M. tuberculosis*, *M. bovis* and *M. bovis* BCG Pasteur, and a novel 12.7 kb segment present in *M. tuberculosis* but absent from *M. bovis* and *M. bovis* BCG was characterized. This region contains
25 a set of genes whose products show low similarity to proteins involved in polysaccharide biosynthesis. The H37Rv BAC library therefore provides the one skilled in the art with a powerful tool both for the generation and confirmation of sequence data as well as for comparative genomics and a plurality of post-genomic applications.

30 [043] The above described BAC-based *Mycobacterium tuberculosis* genomic DNA library is part of the present invention and has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number I-1945.

[044] Another BAC-based DNA library has been constructed with the genomic
35 DNA of *Mycobacterium bovis* BCG, Pasteur strain, and said DNA library has

been deposited ^{June 30} in the Collection Nationale de Cultures de Microorganismes (CNCM) on [XX XX], 1998 under the accession number I-[XXXX] ²⁰⁴⁹

[045] Thus, as a specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library that has been constructed from the genomic DNA of *Mycobacterium tuberculosis*, more specifically of the H37Rv strain and particularly of the DNA library deposited in the accession number I-1945.

[046] In another specific embodiment of the above described method for isolating a polynucleotide of interest said method makes use of at least one BAC-based DNA library has been constructed from the genomic DNA of *Mycobacterium bovis* BCG, more specifically of the Pasteur strain and particularly of the DNA library deposited in the accession number I-[XXXX] ²⁰⁴⁹

[047] In more details, the method according to the invention for isolating a polynucleotide of interest may comprise the following steps :

15 [048] a) isolating at least one polynucleotide contained in a clone of a BAC-based DNA library of mycobacterial origin;

[049] b) isolating :

[050] - at least one genomic or cDNA polynucleotide from a mycobacterium, said mycobacterium belonging to a strain different from the strain used to construct the BAC-based DNA library of step a); or alternatively

20 [051] - at least one polynucleotide contained in a clone of a BAC-based DNA library prepared from the genome of a mycobacterium that is different from the mycobacterium used to construct the BAC-based DNA library of step a);

[052] c) hybridizing the at least one polynucleotide of step a) to the at least one polynucleotide of step b);

25 [053] d) selecting the at least one polynucleotide of step a) that has not formed a hybrid complex with the at least one polynucleotide of step b);

[054] e) characterizing the selected polynucleotide.

[055] Following the above procedure, the at least one polynucleotide of step a) may be prepared as follows :

30 [056] 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease in order to isolate the polynucleotide insert of interest from the vector genetic material;

[057] 2) optionally amplifying the resulting polynucleotide insert;

3) optionally digesting the polynucleotide insert of step 1) or step 2) with at least one restriction endonuclease.

[059] The above method of the invention allows the one skilled in the art to perform comparative genomics between different strains or species of mycobacteria cells, for example between pathogenic strains or species and their non pathogenic strains or species counterparts, as it is the illustrative case for the genomic comparison between *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG that is described herein in the examples.

[060] Restriction digests of a given clone of a BAC library according to the invention may be blotted to membranes, and then probed with radiolabeled DNA from another strain or another species of mycobacteria, allowing the one skilled in the art to identify, characterize and isolate a polynucleotide of interest that may be involved in important metabolic and/or physiological pathways of the mycobacterium under testing, such as a polynucleotide functionally involved in the pathogenicity of said given mycobacteria for its host organism.

[061] More specifically, the inventors have shown in Example 6 that when restriction digests of a given clone of the BAC library identified by the CNCM accession number I-1945 are blotted to membranes and then probed with radiolabeled total genomic DNA from, for example, *Mycobacterium bovis* BCG Pasteur, it is observed that restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA are absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv.

[062] Thus, a further object of the present invention consists in a polynucleotide of interest that has been isolated according to the method described herein before.

[063] In Example 6, a polynucleotide of approximately 12.7 kilobases has been isolated that is present in the genome of *M. tuberculosis* but is absent of the genome of *M. bovis* BCG. This polynucleotide of interest contains 11 ORFs that may be involved in polysaccharide biosynthesis. In particular, two of said ORFs are of particular interest, namely ORF6 (MTCY277.33; Rv1511) that encodes a protein that shares significant homology with bacterial GDP-D-mannose dehydratases, whereas the protein encoded by ORF7 (MTCY277.34; Rv1512) shares significant homology with a nucleotide sugar epimerase. As polysaccharide is a major constituent of the mycobacterial cell wall, these deleted genes may cause the cell wall of *M. bovis* BCG to differ from that of *M. tuberculosis*, a fact that may have important consequences for both the immune

response to *M. bovis* BCG and virulence. Detection of such a polysaccharide is of diagnostic interest and possibly useful in the design of tuberculosis vaccines.

[D64] Consequently, the polynucleotide of interest obtained following the method according to the invention may contain at least one ORF, said ORF
5 preferably encoding all or part of a polypeptide involved in an important
metabolical and/or physiological pathway of the mycobacteria under testing, and
more specifically all or part of a polypeptide that is involved in the pathogenicity
of the mycobacteria under testing, such as for example *Mycobacterium*
tuberculosis, and more generally mycobacteria belonging to the *Mycobacterium*
10 *tuberculosis* complex.

[O65] The *Mycobacterium tuberculosis* complex has its usual meaning, i.e. the
complex of mycobacteria causing tuberculosis which are *Mycobacterium*
tuberculosis, *Mycobacterium bovis*, *Mycobacterium africanum*, *Mycobacterium*
microti and the vaccine strain *Mycobacterium bovis* BCG.

[O66] An illustrative polynucleotide of interest according to the present
15 invention comprises all or part of the polynucleotide of approximately 12.7
kilobases that is present in the genome of *M. tuberculosis* but is absent from the
genome of *M. bovis* BCG disclosed hereinbefore. This polynucleotide is
contained in clone Rv58 of the BAC DNA library I-1945.

20 [O67] Generally, the invention also pertains to a purified polynucleotide
comprising the DNA insert contained in a recombinant BAC vector belonging to
a BAC-based mycobacterial genomic DNA library, such as for example the I-
1945 BAC DNA library.

[O68] Advantageously, such a polynucleotide has been identified according to
25 the method of the invention.

[O69] Such a polynucleotide of interest may be used as a probe or a primer
useful for specifically detecting a given mycobacterium of interest, such as
Mycobacterium tuberculosis or *Mycobacterium bovis* BCG.

[D70] More specifically, the invention then deals with a purified polynucleotide
30 useful as probe or a primer comprising all or part of the nucleotide sequence SEQ
ID N°1.

[D71] The location, on the *Mycobacterium tuberculosis* chromosome, of the
above polynucleotide of sequence SEQ ID N°1 has now been ascribed to begin,
at its 5' end at nucleotide at position nt 1696015 and to end, at its 3' end, at
35 nucleotide at position nt 1708746.

[072] For diagnostic purposes, this 12.7 kb deletion should allow a rapid PCR screening of tubercle isolates to identify whether they are bovine or human strains. The primers listed in Table 1 are flanking the deleted region and give a 722 bp amplicon in *M. bovis* or *M. bovis* BCG strains, but a fragment of 13,453 bp in *M. tuberculosis* that is practically impossible to amplify under the same PCR conditions. More importantly, assuming that some of the gene products from this region represent proteins with antigenic properties, it could be possible to develop a test that can reliably distinguish between the immune response induced by vaccination with *M. bovis* BCG vaccine strains and infection with *M. tuberculosis* or that the products (e.g. polysaccharides) are specific immunogens.

[073] The invention also provides for a purified polynucleotide useful as a probe or as a primer, said polynucleotide being chosen in the following group of polynucleotides :

[074] a) a polynucleotide comprising at least 8 consecutive nucleotides of the sequence
15 SEQ ID N°1;

[075] b) a polynucleotide whose sequence is fully complementary to the sequence of the polynucleotide defined in a);

[076] c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

[077] For the purpose of defining a polynucleotide or oligonucleotide hybridizing under stringent hybridization conditions, such as above, it is intended a polynucleotide that hybridizes with a reference polynucleotide under the following hybridization conditions.

[078] The hybridization step is realized at 65°C in the presence of 6 x SSC buffer, 5 x Denhardt's solution, 0,5% SDS and 100µg/ml of salmon sperm DNA.

[079] For technical information, 1 x SSC corresponds to 0.15 M NaCl and 0.05M sodium citrate; 1 x Denhardt's solution corresponds to 0.02% Ficoll, 0.02% polyvinylpyrrolidone and 0.02% bovine serum albumin.

[080] The hybridization step is followed by four washing steps :

[081] two washings during 5 min, preferably at 65°C in a 2 x SSC and 0.1%SDS buffer,

[082] - one washing during 30 min, preferably at 65°C in a 2 x SSC and 0.1% SDS buffer,

[083] - one washing during 10 min, preferably at 65°C in a 0.1 x SSC and 0.1%SDS buffer.

[084] A first illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°2 that corresponds to the Sp6 end-sequence of SEQ ID N°1.

5 [085] A second illustrative useful polynucleotide that is included in the polynucleotide of sequence SEQ ID N°1 is the polynucleotide of sequence SEQ ID N°3 that corresponds to the T7 end-sequence of SEQ ID N°1, located on the opposite strand.

10 [086] The polynucleotide of sequence SEQ ID N°1 contains 11 ORFs, the respective locations of which, taking into account the orientation of each ORF on the chromosome, on the sequence of the *Mycobacterium tuberculosis* chromosome, is given hereafter :

[087] - The location of ORF1 is comprised between nucleotide at position nt 1695944 and nucleotide at position nt1696441.

15 [088] - The location of ORF2 is comprised between nucleotide at position nt 1696728 and nucleotide at position nt1697420.

[089] - The location of ORF3 is comprised between nucleotide at position nt 1698096 and nucleotide at position nt1699892. ORF3 probably encodes a protein having the characteristics of a membrane protein.

20 [090] - The location of ORF4 is comprised between nucleotide at position nt 1700210 and nucleotide at position nt1701088.

[091] - The location of ORF5 is comprised between nucleotide at position nt 1701293 and nucleotide at position nt1702588. ORF5 encodes a protein having the characteristics of a membrane protein.

25 [092] - The location of ORF6 is comprised between nucleotide at position nt 1703072 and nucleotide at position nt1704091. ORF6 encodes a protein having the characteristics of a GDP-D-mannose dehydratase.

30 [093] - The location of ORF7 is comprised between nucleotide at position nt 1704091 and nucleotide at position nt1705056. ORF7 encodes a protein having the characteristics of a nucleotide sugar epimerase involved in colanic acid biosynthesis.

[094] - The location of ORF8 is comprised between nucleotide at position nt 1705056 and nucleotide at position nt1705784.

35 [095] - The location of ORF9 is comprised between nucleotide at position nt 1705808 and nucleotide at position nt1706593. ORF9 encodes a protein having the characteristics of colanic acid biosynthesis glycosyl transferase.

[096] - The location of ORF10 is comprised between nucleotide at position nt 1706631 and nucleotide at position nt1707524.

[097] - The location of ORF11 is comprised between nucleotide at position nt 1707530 and nucleotide at position nt1708648. ORF11 encodes a protein similar to a spore coat polysaccharide biosynthesis.

[098] A polynucleotide of interest obtained by the above-disclosed method according to the invention may also contain at least one ORF that encodes all or part of acidic, glycine-rich proteins, belonging to the PE and PPE families, whose genes are often clustered and based on multiple copies of the polymorphic repetitive sequences. The names PE and PPE derive from the fact that the motifs ProGlu (PE, positions 8, 9) and ProProGlu (PPE, positions 7 to 9) are found near the N-terminus in almost all cases. The PE protein family all have a highly conserved N-terminal domain of ~110 amino acid residues, that is predicted to have a globular structure, followed by a C-terminal segment which varies in size, sequence and repeat copy number. Phylogenetic analysis separated the PE family into several groups, the larger of which is the highly repetitive PGRS class containing 55 members whereas the other groups share very limited sequence similarity in their C-terminal domains. The predicted molecular weights of the PE proteins vary considerably as a few members only contain the ~110 amino acid N-terminal domain while the majority have C-terminal extensions ranging in size from 100 up to >1400 residues. A striking feature of the PGRS proteins is their exceptional glycine content (up to 50%) due to the presence of multiple tandem repetitions of GlyGlyAla or GlyGlyAsn motifs or variations thereof.

[099] Like the PE family, the PPE protein family also has a conserved N-terminal domain that comprises ~180 amino acid residues followed by C-terminal segments that vary considerably in sequence and length. These proteins fall into at least three groups, one of which constitutes the MPTR class characterised by the presence of multiple, tandem copies of the motif AsnXGlyXGlyAsnXGly. The second subgroup contains a characteristic, well-conserved motif around position 350 (GlyXXSerValProXXTrp) whereas the other group contains proteins that are unrelated except for the presence of the common 180-residue PPE domain. C-terminal extensions may range in size from 00 up to 3500 residues.

[0100] One member of the PGRS sub-family, the WHO antigen 22T (Abou-Zeid et al., 1991), a 55kD protein capable of binding fibronectin, is produced during

disease and elicits a variable antibody response suggesting either that individuals mount different immune responses or that this PGRS-protein may not be produced in this form by all strains of *M. tuberculosis*. In other words, at least some PE_PGRS coding sequences encode for proteins that are involved in the recognition of *M. tuberculosis* by the immune system of the infected host. Therefore, differences in the PGRS sequences could represent the principal source of antigenic variation in the otherwise genetically and antigenically homogeneous bacterium.

[0101] By performing the method of the invention using the *M. tuberculosis* BAC based DNA library I-1945, the inventors have discovered the occurrence of sequence differences between a given PGRS encoding ORF (ORF reference on the genomic sequence of *M. tuberculosis* Rv0746) of *M. tuberculosis* and its counterpart sequence in the genome of *M. bovis* BCG.

[0102] More precisely, the inventors have determined that one ORF contained in BAC vector N° Rv418 of the *M. tuberculosis* BCG I-1945 DNA library carries both base additions and base deletions when compared with the corresponding ORF in the genome of *M. bovis* BCG that is contained in the BAC vector N° X0175 of the *M. bovis* BCG I-XXXX DNA library. The variations observed in the base sequences correspond to variations in the C-terminal part of the amino acid sequence of the PGRS ORF translation product.

[0103] As shown in Figure 6, an amino acid stretch of 9 residues in length is present in this *M. tuberculosis* PGRS (ORF reference Rv0746) and is absent from the ORF counterpart of *M. bovis* BCG, namely the following amino acid sequence:

25 [0104] NH₂-GGAGGAGGSSAGGGGAGGAGGWLLGD-COOH (SEQ ID NO. 732)

[0105] Furthermore, Figure 6 shows also that an amino acid stretch of 45 residues in length is absent from this *M. tuberculosis* PGRS and is present in the ORF counterpart of *M. bovis* BCG, namely following amino acid sequence:

[0106] NH₂-GAGGIGGIGGNANGGAGGNGGTGGQLWGSGGAGVEGGAAL
30 SVGDT-COOH (SEQ ID NO. 733)

[0107] Similar observations were made with PPE ORF Rv0442, which showed a 5 codon deletion relative to a *M. bovis* amino acid sequence.

[0108] Given that the polymorphism associated with the PE-PGRS or PEE ORFS resulted in extensive antigenic variability or reduced antigen presentation, this would be of immense significance for vaccine design, for understanding

protective immunity in tuberculosis and, possibly, explain the varied responses seen in different BCG vaccination programmes.

[0109] There are several striking parallels between the PGRS proteins and the Epstein-Barr virus-encoded nuclear antigens (EBNA). Both polypeptide families are glycine-rich, contain Gly-Ala repeats that represent more than one third of the molecule, and display variation in the length of the repeat region between different isolates. The Gly-Ala repeat region of EBNA1 has been shown to function as a *cis*-acting inhibitor of antigen processing and MHC class I-restricted antigen presentation (Levitskaya et al., 1995). The fact that MHC class I knock-out mice are extremely susceptible to *M. tuberculosis* underlines the importance of MHC class I antigen presentation in protection against tuberculosis. Therefore, it is possible that the PE/PPE protein family also play some role in inhibiting antigen presentation, allowing the bacillus to hide from the host's immune system.

[0110] As such the novel and nonobvious PGRS polynucleotide from *M. bovis* which is homolog to the *M. tuberculosis* ORF Rv0746, and which is contained in the BAC clone N° X0175 (See Table 4 for SP6 and T7 end-sequences of clone n° X0175) of the I-~~XXXX~~⁽²⁰⁴⁹⁾ *M. bovis* BCG BAC DNA library is part of the present invention, as it represents a starting material in order to define specific probes or primers useful for detection of antigenic variability in mycobacterial strains, possible inhibition of antigen processing as well as to differentiate *M. tuberculosis* from *M. bovis* BCG.

[0111] Thus, a further object of the invention consists in a polynucleotide comprising the sequence SEQ ID N°4.

[0112] Polynucleotides of interest have been defined by the inventors as useful detection tools in order to differentiate *M. tuberculosis* from *M. bovis* BCG. Such polynucleotides are contained in the 45 aminoacid length coding sequence that is present in *M. bovis* BCG but absent from *M. tuberculosis*. This polynucleotide has a sequence beginning (5'end) at the nucleotide at position nt 729 of the sequence SEQ ID N°4 and ending (3'end) at the nucleotide in position nt 863 of the sequence SEQ ID N°4.

[0113] Thus, part of the present invention is also a polynucleotide which is chosen among the following group of polynucleotides :

[0114] a) a polynucleotide comprising at least 8 consecutive nucleotides of the nucleotide sequence SEQ ID N°5 ;

[0115] b) a polynucleotide which sequence is fully complementary to the sequence of the polynucleotide defined in a) ;

[0116] c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

5 [0117] The stringent hybridization conditions for the purpose of defining the above disclosed polynucleotide are defined herein before in the specification.

[0118] The invention also provides for a BAC-based *Mycobacterium tuberculosis* strain H37Rv genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes on November 19, 1997 under the
10 accession number I-1945.

[0119] A further object of the invention consists in a recombinant BAC vector which is chosen among the group consisting of the recombinant BAC vectors belonging to the BAC-based DNA library I-1945.

[0120] Generally, a recombinant BAC vector of interest may be chosen among
15 the following set or group of BAC vectors contained in the BAC-based DNA library I-1945 :

[0121] Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv10;
Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119;
Rv11; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129;
20 Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv13; Rv140;
Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv14;
Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv15;
Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv16;
Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179;
25 Rv17; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188;
Rv18; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv19; Rv1; Rv201;
Rv204; Rv205; Rv207; Rv209; Rv20; Rv214; Rv215; Rv217; Rv218; Rv219;
Rv21; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228;
Rv229; Rv22; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240;
30 Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv24; Rv251; Rv252;
Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv25; Rv260; Rv261; Rv262;
Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv26; Rv270; Rv271;
Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv27; Rv280;
Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv28;
35 Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv29; Rv2; Rv301;

Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv30; Rv310; Rv311;
 Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv31; Rv32;
 Rv322; Rv327; Rv328; Rv329; Rv32; Rv330; Rv331; Rv333; Rv334; Rv335;
 Rv336; Rv337; Rv338; Rv339; Rv33; Rv340; Rv341; Rv343; Rv344; Rv346;
 5 Rv347; Rv348; Rv349; Rv34; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355;
 Rv356; Rv357; Rv358; Rv359; Rv35; Rv360; Rv361; Rv363; Rv364; Rv365;
 Rv366; Rv367; Rv368; Rv369; Rv36; Rv370; Rv371; Rv373; Rv374; Rv375;
 Rv376; Rv377; Rv378; Rv379; Rv37; Rv381; Rv382; Rv383; Rv384; Rv385;
 Rv386; Rv387; Rv388; Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396;
 10 Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419;
 Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51;
 Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62;
 Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73;
 Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84;
 15 Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96;
 Rv9.

[0122] The end sequences of the polynucleotide inserts of each of the above clones corresponding respectively to the sequences adjacent to the T7 promoter and to the Sp6 promoter on the BAC vector are shown in Table 3.

20 [0123] It has been shown by the inventors that the minimal overlapping set of BAC vectors of the BAC-based DNA library I-1945 contains 68 unique BAC clones and practically spans almost the whole H37Rv chromosome with the exception of a single gap of approximately 150 kb.

[0124] More specifically, a recombinant BAC vector of interest is chosen among
 25 the following set or group of BAC vectors from the BAC-based DNA library I-1945, the location of which vector DNA inserts on the chromosome of *M. tuberculosis* is shown in Figure 3 :

[0125] Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228;
 Rv233; Rb38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3;
 30 Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222;
 Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60;
 Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56;
 Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121;
 Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270;
 35 Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407;

Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417; Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86; Rv412; Rv73; Rv269; Rv214; Rv287; Rv42; Rv143.

[0126] The polynucleotides disclosed in Table 3 may be used as probes in order
5 to select a given clone of the BAC DNA library I-1945 for further use.

[0127] The invention also provides for a BAC-based *Mycobacterium bovis* strain
Pasteur genomic DNA library that has been deposited in the Collection Nationale
de Cultures de Microorganismes on [XXXX XX], 1998 under the accession
number I-[XXXX] ²⁰⁴⁹ June 30

10 [0128] A further object of the invention consists in a recombinant BAC vector
which is chosen among the group consisting of the recombinant BAC vectors
belonging to the BAC-based DNA library I-[XXXX] ²⁰⁴⁹. This DNA library contains
approximately 1600 clones. The average insert size is estimated to be ~80 kb.

[0129] Generally, a recombinant BAC vector of interest may be chosen among
15 the following set or group of BAC vectors contained in the BAC-based DNA
library I-[XXXX] ²⁰⁴⁹

[0130] X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012;
X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021; X0175.

[0131] The end sequences of the polynucleotide inserts of each of the above
20 clones corresponding respectively to the sequences adjacent to the T7 promoter
and to the Sp6 promoter on the BAC vector are shown in Table 4.

[0132] The polynucleotides disclosed in Table 4 may be used as probes in order
to select a given clone of the BAC DNA library I-[XXXX] ²⁰⁴⁹ for further use.

[0133] Are also part of the invention the polynucleotide inserts that are contained
25 in the above described BAC vectors, that are useful as primers or probes.

[0134] These polynucleotides and nucleic acid fragments may be used as primers
for use in amplification reactions, or as nucleic probes.

[0135] PCR is described in the US patent N° 4,683,202. The amplified fragments
may be identified by an agarose or a polyacrylamide gel electrophoresis, or by a
30 capillary electrophoresis or alternatively by a chromatography technique (gel
filtration, hydrophobic chromatography or ion exchange chromatography). The
specificity of the amplification may be ensured by a molecular hybridization
using, for example, one of the initial primers as nucleic probes.

[0136] Amplified nucleotide fragments are used as probes in hybridization
35 reactions in order to detect the presence of one polynucleotide according to the

present invention or in order to detect mutations in the genome of the given mycobacterium of interest, specifically a mycobacterium belonging to the *Mycobacterium tuberculosis* complex and more specifically *Mycobacterium tuberculosis* and *Mycobacterium bovis* BCG.

5 [0137] Are also part of the present invention the amplified nucleic fragments (« amplicons ») defined herein above.

[0138] These probes and amplicons may be radioactively or non-radioactively labeled, using for example enzymes or fluorescent compounds.

10 [0139] Other techniques related to nucleic acid amplification may also be used and are generally preferred to the PCR technique.

[0140] The Strand Displacement Amplification (SDA) technique (Walker et al., 1992) is an isothermal amplification technique based on the ability of a restriction enzyme to cleave one of the strands at his recognition site (which is under a hemiphosphorothioate form) and on the property of a DNA polymerase
15 to initiate the synthesis of a new strand from the 3'OH end generated by the restriction enzyme and on the property of this DNA polymerase to displace the previously synthesized strand being localized downstream. The SDA method comprises two main steps :

[0141] a) The synthesis, in the presence of dCTP- α -S, of DNA molecules that are
20 flanked by the restriction sites that may be cleaved by an appropriate enzyme.

[0142] b) The exponential amplification of these DNA molecules modified as such, by enzyme cleavage, strand displacement and copying of the displaced strands. The steps of cleavage, strand displacement and copy are repeated a sufficient number of times in order to obtain an accurate sensitivity of the assay.

25 [0143] The SDA technique was initially realized using the restriction endonuclease HincII but is now generally practised with an endonuclease from *Bacillus stearothermophilus* (BSOBI) and a fragment of a DNA polymerase which is devoid of any 5'→3' exonuclease activity isolated from *Bacillus cladothensis* (exo- Bca) [=exo-minus-Bca]. Both enzymes are able to operate at
30 60°C and the system is now optimized in order to allow the use of dUTP and the decontamination by UDG. When using this technique, as described by Spargo et al. in 1996, the doubling time of the target DNA is of 26 seconds and the amplification rate is of 10^{10} after an incubation time of 15 min at 60°C.

[0144] The SDA amplification technique is more easy to perform than PCR (a single thermostated waterbath device is necessary) and is faster than the other amplification methods.

[0145] Thus, another object of the present invention consists in using the nucleic acid fragments according to the invention (primers) in a method of DNA or RNA amplification according to the SDA technique. For performing SDA, two pairs of primers are used : a pair of external primers (B1, B2) consisting of a sequence specific for the target polynucleotide of interest and a pair of internal primers (S1, S2) consisting of a fusion oligonucleotide carrying a site that is recognized by a restriction endonuclease, for example the enzyme BSOBI.

[0146] The operating conditions to perform SDA with such primers are described in Spargo et al, 1996.

[0147] The polynucleotides of the invention and their above described fragments, especially the primers according to the invention, are useful as technical means for performing different target nucleic acid amplification methods such as :

[0148] - TAS (Transcription-based Amplification System), described by Kwoh et al. in 1989.

[0149] - SR (Self-Sustained Sequence Replication), described by Guatelli et al. in 1990.

[0150] - NASBA (Nucleic acid Sequence Based Amplification), described by Kievitis et al. in 1991.

[0151] - TMA (Transcription Mediated Amplification).

[0152] The polynucleotides according to the invention are also useful as technical means for performing methods for amplification or modification of a nucleic acid used as a probe , such as :

[0153] LCR (Ligase Chain Reaction), described by Landegren et al. in 1988 and improved by Barany et al. in 1991 who employ a thermostable ligase.

[0154] - RCR (Repair Chain Reaction) described by Segev et al. in 1992.

[0155] - CPR (Cycling Probe Reaction), described by Duck et al. in 1990.

[0156] - Q-beta replicase reaction, described by Miele et al. in 1983 and improved by Chu et al. in 1986, Lizardi et al. in 1988 and by Burg et al. and Stone et al. in 1996.

[0157] When the target polynucleotide to be detected is a RNA, for example a mRNA, a reverse transcriptase enzyme will be used before the amplification reaction in order to obtain a cDNA from the RNA contained in the biological sample. The generated cDNA is subsequently used as the nucleic acid target for

the primers or the probes used in an amplification process or a detection process according to the present invention.

[0158] The non-labeled polynucleotides or oligonucleotides of the invention may be directly used as probes. Nevertheless, the polynucleotides or oligonucleotides
5 are generally labeled with a radioactive element (^{32}P , ^{35}S , ^3H , ^{125}I) or by a non-isotopic molecule (for example, biotin, acetylaminofluorene, digoxigenin, 5-bromodesoxyuridin, fluorescein) in order to generate probes that are useful for numerous applications.

[0159] Examples of non-radioactive labeling of nucleic acid fragments are
10 described in the french patent N° FR-7810975 or by Urdea et al. or Sanchez-Pescador et al., 1988.

[0160] In the latter case, other labeling techniques may be also used such as those described in the french patents FR-2 422 956 and 2 518 755. The hybridization step may be performed in different ways (Matthews et al., 1988). The more
15 general method consists of immobilizing the nucleic acid that has been extracted from the biological sample onto a substrate (nitrocellulose, nylon, polystyrene) and then to incubate, in defined conditions, the target nucleic acid with the probe. Subsequently to the hybridization step, the excess amount of the specific probe is discarded and the hybrid molecules formed are detected by an appropriate
20 method (radioactivity, fluorescence or enzyme activity measurement).

[0161] Advantageously, the probes according to the present invention may have structural characteristics such that they allow the signal amplification, such structural characteristics being, for example, branched DNA probes as those described by Urdea et al. in 1991 or in the European patent N° EP-0 225 807
25 (Chiron).

[0162] In another advantageous embodiment of the probes according to the present invention, the latters may be used as « capture probes », and are for this purpose immobilized on a substrate in order to capture the target nucleic acid contained in a biological sample. The captured target nucleic acid is subsequently
30 detected with a second probe which recognizes a sequence of the target nucleic acid which is different from the sequence recognized by the capture probe.

[0163] The oligonucleotide probes according to the present invention may also be used in a detection device comprising a matrix library of probes immobilized on a substrate, the sequence of each probe of a given length being localized in a shift
35 of one or several bases, one from the other, each probe of the matrix library thus

being complementary to a distinct sequence of the target nucleic acid. Optionally, the substrate of the matrix may be a material able to act as an electron donor, the detection of the matrix positions in which an hybridization has occurred being subsequently determined by an electronic device. Such matrix libraries of probes
5 and methods of specific detection of a target nucleic acid is described in the European patent application N° EP-0 713 016 (Affymax technologies) and also in the US patent N° US-5,202,231 (Drmanac).

[0164] Since almost the whole length of a mycobacterial chromosome is covered by a BAC-based genomic DNA libraries according to the present invention (i.e. 97% of
10 the *M. tuberculosis* chromosome is covered by the BAC library I-1945), these DNA libraries will play an important role in a plurality of post-genomic applications, such as in mycobacterial gene expression studies where the canonical set of BACs could be used as a matrix for hybridization studies. Probing such matrices with cDNA probes prepared from total mRNA will uncover genetic loci induced or repressed
15 under different physiological conditions (Chuang et al., 1993; Trieselmann et al., 1992). As such, the H37Rv BAC library represents a fundamental resource for present and future genomics investigations.

[0165] The BAC vectors or the polynucleotide inserts contained therein may be directly used as probes, for example when immobilized on a substrate such as
20 described herein before.

[0166] The BAC vectors or their polynucleotide inserts may be directly adsorbed on a nitrocellulose membrane, at predetermined locations on which one or several polynucleotides to be tested are then put to hybridize therewith.

[0167] Preferably, a collection of BAC vectors that spans the whole genome of
25 the mycobacterium under testing will be immobilized, such as, for example, the set of 68 BAC vectors of the I-1945 DNA library that is described elsewhere in the specification and shown in Figure 3.

[0168] The immobilization and hybridization steps may be performed as described in the present Materials and Methods Section.

[0169] As another illustrative embodiment of the use of the BAC vectors of the
30 invention as polynucleotide probes, these vectors may be useful to perform a transcriptional activity analysis of mycobacteria growing in different environmental conditions, for example under conditions in which a stress response is expected, as it is the case at an elevated temperature, for example
35 40°C.

[0170] In this specific embodiment of the invention, Genescreen membranes may be used to immobilize the restriction endonuclease digests (*Hind*III digests for the BAC DNA library I-1945) of the BAC vectors by transfer from a gel (Trieselmann et al., 1992).

5 [0171] Alternatively, the BAC vectors may be immobilized for dot blot experiments as follows. First, the DNA concentration of each BAC clone is determined by hybridization of blots of clone DNAs and of a BAC vector concentration standard with a BAC vector specific DNA probe. Hybridization is quantified by the Betascope 603 blot analyzer (Betagen Corp.), which collects
10 beta particles directly from the blot with high efficiency. Then, 0.5 µg of each clone DNA is incubated in 0.25 M NaOH and 10 mM EDTA at 65°C for 60 min to denature the DNA and degrade residual RNA contaminants. By using a manifold filtration system (21 by 21 wells), each clone DNA is blotted onto a GeneScreen Plus nylon membrane in the alkaline solution. After neutralization,
15 the blots are baked at 85°C for 2 h under vacuum. Positive and negative controls are added when necessary. In order to perform this procedure, it may be referred to the article of Chuang et al. (1993).

[0172] For RNA extractions, cells grown in a suitable volume of culture medium may, for example, be immediately mixed with an equal volume of crushed ice at -
20 70°C and spun at 4°C in a 50 ml centrifugation tube. The cell pellet is then suspended in 0.6 ml of ice-cold buffer (10 mM KCl, 5 mM MgCl, 10 mM Tris; pH 7.4) and then immediately added to 0.6 ml of hot lysis buffer (0.4 M NaCl, 40 mM EDTA, 1% beta-mercaptoethanol, 1% SDS, 20 mM Tris; pH 7.4) containing 100 µl of water saturated phenol. This mixture is incubated in a boiling water
25 bath for 40 s. The debris are removed by centrifugation. The supernatant is extracted with phenol-chloroform five times, ethanol precipitated, and dried. The dried RNA pellet is dissolved in water before use.

[0173] Then labeled total cDNA may be prepared by the following method. The reaction mixture contains 15 µg of the previously prepared total RNA, 5 µg of
30 pd(N₆) (random hexamers from Pharmacia Inc.), 0.5 mM dATP, 0.5 mM dGTP and 0.5mM DTTP, 5µM dCTP, 100 µCi of [α -³²P]dCTP (3,000 Ci/mmol), 50 mM Tris-HCl (pH 8.3), 6 mM MgCl₂, 40 mM KCl, 0.5 U of avian myeloblastosis virus reverse transcriptase (Life Science Inc.) in a total volume of 50 µl. The reaction is allowed to continue overnight at room temperature. EDTA and NaOH
35 are then added to final concentrations of 50 mM and 0.25 M, respectively, and

the mixture is incubated at 65°C for 30 min to degrade the RNA templates. The cDNA is then ready to use after neutralization by adding Hcl and Tris buffer.

[0174] The hybridization step may be performed as described by Chuang et al. (1993) and briefly disclosed hereinafter. The DNA dot blot is hybridized to ³²P-labeled total cDNA in a solution containing 0.1% polyvinylpyrrolidone, 0.1% Ficoll, 0.1% sodium P_{pi}, 0.1% bovine serum albumin, 0.5% SDS, 100 mM NaCl, and 0.1 mM sodium citrate, pH 7.2, at 65°C for 2 days and then washed with a solution containing 0.1% SDS, 100 mM NaCl, and 10 mM Na-citrate, pH 7.2. The same dot blot is used for hybridization with both control and experimental cDNAs, with an alkaline probe stripping procedure (soaked twice in 0.25M NaOH-0.75 M NaCl at room temperature, 30 min each, neutralized, and completely dried at 65°C for at least 30 min) between the two hybridizations. Quantification may be done with the Betascope 603 blot analyzer (Betagen Corp.).

15 [0175] As it flows from the above technical teachings, another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

[0176] a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention with a biological sample ;

[0177] 20 b) detecting the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid molecules contained within the biological sample.

[0178] The invention further deals with a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

[0179] 25 a) bringing into contact the recombinant BAC vector or a purified polynucleotide according to the invention that has been immobilized onto a substrate with a biological sample ;

[0180] b) bringing into contact the hybrid nucleic acid molecule formed between said purified polynucleotide and the nucleic acid contained in the biological sample with a labeled recombinant BAC vector or a polynucleotide according to the invention, provided that said polynucleotide and polynucleotide of step a) have non-overlapping sequences.

30 [0181] Another object of the invention consists in a method for detecting the presence of mycobacteria in a biological sample comprising the steps of :

- [0182] a) bringing into contact the nucleic acid molecules contained in the biological sample with a pair of primers according to the invention;
- [0183] b) amplifying said nucleic acid molecules;
- [0184] c) detecting the nucleic acid fragments that have been amplified, for example by
5 gel electrophoresis or with a labeled polynucleotide according to the invention.
- [0185] In one specific embodiment of the above detection and/or amplification methods, said methods comprise an additional step wherein before step a), the nucleic acid molecules of the biological sample have been made available to a hybridization reaction.
- 10 [0186] In another specific embodiment of the above detection methods, said methods comprise an additional step, wherein, before the detection step, the nucleic acid molecules that are not hybridized with the immobilized purified polynucleotide are removed.
- [0187] Also part of the invention is a kit for detecting mycobacteria in a
15 biological sample comprising :
- [0188] a) a recombinant BAC vector or a purified polynucleotide according to the invention;
- [0189] b) reagents necessary to perform a nucleic acid hybridization reaction.
- [0190] The invention also pertains to a kit for detecting a mycobacteria in a
20 biological sample comprising :
- [0191] a) a recombinant BAC vector or a purified polynucleotide according to the invention that is immobilized onto a substrate;
- [0192] b) reagents necessary to perform a nucleic acid hybridization reaction;
- [0193] c) a purified polynucleotide according to the invention which is radioactively or
25 non-radioactively labeled, provided that said polynucleotide and the polynucleotide of step a) have non-overlapping sequences.
- [0194] Moreover, the invention provides for a kit for detecting mycobacteria in a biological sample comprising :
- [0195] a) a pair of purified primers according to the invention;
- [0196] 30 b) reagents necessary to perform a nucleic acid amplification reaction;
- [0197] c) optionally, a purified polynucleotide according to the invention useful as a probe.
- [0198] The invention embraces also a method for detecting the presence of a genomic DNA, a cDNA or a mRNA of mycobacteria in a biological sample,
35 comprising the steps of :

[0199] a) bringing into contact the biological sample with a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention, that are immobilized on a substrate;

[0200] b) detecting the hybrid complexes formed.

5 [0201] The invention also provides a kit for detecting the presence of genomic DNA, cDNA or mRNA of a mycobacterium in a biological sample, comprising :

[0202] a) a substrate on which a plurality of BAC vectors according to the invention or purified polynucleotides according to the invention have been immobilized;

[0203] b) optionally, the reagents necessary to perform the hybridization reaction.

10 [0204] Additionally, the recombinant BAC vectors according to the invention and the polynucleotide inserts contained therein may be used for performing detection methods based on « molecular combing ». Said methods consist in methods for aligning macromolecules, especially DNA and are applied to processes for detecting, for measuring intramolecular distance, for separating and/or for
15 assaying a macromolecule, especially DNA in a sample.

[0205] These « molecular combing » methods are simple methods, where the triple line S/A/B (meniscus) resulting from the contact between a solvent A and the surface S and a medium B is caused to move on the said surface S, the said macromolecules (i.e. DNA) having a part, especially an end, anchored on the
20 surface S, the other part, especially the other end, being in solution in the solvent A. These methods are particularly fully described in the PCT Application n° PCT/FR 95/00165 filed on February 11, 1994 (Bensimon et al.).

[0206] When performing the « molecular combing » method with the recombinant BAC vectors according to the inventions or their polynucleotide inserts, the
25 latters may be immobilized (« anchored ») on a suitable substrate and aligned as described in the PCT Application n° PCT/FR 95/00165, the whole teachings of this PCT Application being hereby incorporated by reference. Then, polynucleotides to be tested, preferably under the form of radioactively or non radioactively labeled polynucleotides, that may consist of fragments of genomic
30 DNA, cDNA etc. are brought into contact with the previously aligned polynucleotides according to the present invention and then their hybridization position on the aligned DNA molecules is determined using any suitable means including a microscope or a suitable camera device.

[0207] Thus, the present invention is also directed to a method for the detection
35 of the presence of a polynucleotide of mycobacterial origin in a biological sample

and/or for physical mapping of a polynucleotide on a genomic DNA, said method comprising :

- [0208] a) aligning at least one polynucleotide contained in a recombinant BAC vector according to the invention on the surface of a substrate;
- [0209] 5 b) bringing into contact at least one polynucleotide to be tested with the substrate on which the at least one polynucleotide of step a) has been aligned;
- [0210] c) detecting the presence and/or the location of the tested polynucleotide on the at least one aligned polynucleotide of step a).

[0211] The invention finally provides for a kit for performing the above method,
10 comprising :

- [0212] a) a substrate whose surface has at least one polynucleotide contained in a recombinant BAC vector according to the invention;
- [0213] b) optionally, reagents necessary for labeling DNA;
- [0214] c) optionally, reagents necessary for performing a hybridization reaction.

15 [0215] In conclusion, it may be underlined that the alliance of such BAC-based approaches such as described in the present specification to the advances in comparative genomics by the availability of an increased number of complete genomes, and the rapid increase of well-characterized gene products in the public databases, will allow the one skilled in the art an exhaustive analysis of the
20 mycobacterial genome.

MATERIALS AND METHODS

- [0216] 1. **DNA-preparation.** Preparation of *M. tuberculosis* H37Rv DNA in agarose plugs was conducted as previously described (Canard et al., 1989; Philipp et al.,
25 1996b). Plugs were stored in 0.2 M EDTA at 4°C and washed 3 times in 0.1% Triton X-100 buffer prior to use.
- [0217] 2. **BAC vector preparation.** pBeloBAC11 was kindly provided by Dr. Shizuya, Department of Biology, California Institute of Technology (Pasadena, CA). The preparation followed the description of Woo et al., 1994 (Woo et al., 1994).
- [0218] 30 3. **Partial digestion with *Hind*III.** Partial digestion was carried out on plugs, each containing approximately 10 µg of high molecular weight DNA, after three one hour equilibration steps in 50 ml of *Hind*III 1X digestion buffer (Boehringer Mannheim, Mannheim, Germany) plus 0.1% Triton X-100. The buffer was then removed and replaced by 1ml/plug of ice-cold *Hind*III enzyme buffer containing
35 20 units of *Hind*III (Boehringer). After two hours incubation on ice, the plugs

were transferred to a 37°C water bath for 30 minutes. Digestions were stopped by adding 500 µl of 50 mM EDTA (pH 8.0).

[0219] 4. Size selection. The partially digested DNA was subjected to contour-clamped homogenous electric field (CHEF) electrophoresis on a 1% agarose gel using a BioRad DR III apparatus (BioRad, Hercules, CA) in 1X TAE buffer at 13°C, with a ramp from 3 to 15 seconds at 6 V/cm for 16 hours. Agarose slices from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were excised from the gel and stored in TE at 4°C.

[0220] 5. Ligation and transformation. Agarose-slices containing fractions from 25 to 75 kb, 75 to 120 kb and 120 to 180 kb were melted at 65°C for 10 minutes and digested with Gelase (Epicentre Technologies, Madison, WI), using 1 unit per 100 µl gel-slice. 25-100 ng of the size-selected DNA was then ligated to 10 ng of *Hind*III digested, dephosphorylated pBeloBAC11 in a 1:10 molar ratio using 10 units of T4 DNA ligase (New England Biolabs, Beverly, MA) at 16°C for 20 hours. Ligation mixtures were heated at 65°C for 15 minutes, then drop-dialysed against TE using Millipore VS 0.025 mM membranes (Millipore, Bedford, MA). Fresh electrocompetent *E. coli* DH10B cells (Sheng et al., 1995) were harvested from 200 ml of a mid-log (OD₅₅₀=0.5) culture grown in SOB medium. Cells were washed three times in ice-cold water, and finally resuspended in ice-cold water to a cell density of 10¹¹ cells/ml (OD₅₅₀=150). 1 µl of the ligation-mix was used for electroporation of 30 µl of electrocompetent DH10B *E. coli* using a Eurogentec Easyject Plus electroporator (Eurogentec, Seraing, Belgium), with settings of 2.5 kV, 25 µF, and 99 Ω, in 2 mm wide electroporation cuvettes. After electroporation, cells were resuspended in 600 µl of SOC medium, allowed to recover for 45 minutes at 37°C with gentle shaking, and then plated on LB agar containing 12.5 µg/ml chloramphenicol (CM), 50 µg/ml X-gal, and 25 µg/ml IPTG. The plates were incubated overnight and recombinants (white colonies) were picked manually to 96 well plates. Each clone was inoculated 3 times (2 X 200 µl and 1 X 100 µl of 2YT/12.5 µg/ml CM per clone) and incubated overnight. One of the microtiter plates, containing 100 µl culture per well, was maintained as a master plate at -80°C after 100 ml of 80% glycerol were added to each well, while minipreps (Sambrook et al., 1989) were prepared from the remaining two plates to check for the presence of inserts. Clones containing inserts were then designated "Rv" clones, repicked from the master plate to a second set of plates for storage of the library at -80°C.

- [0221] 6. Preparation of DNA for sizing, direct sequencing and comparative genomics. A modified Birnboim and Doly protocol (Birnboim et al., 1979) was used for extraction of plasmid DNA for sequencing purposes. Each Rv clone was inoculated into a 50 ml Falcon polypropylene tube containing 40 ml of 2YT medium with 12.5 µg/ml of CM and grown overnight at 37°C with shaking. Cells were harvested by centrifugation and stored at -20°C. The frozen pellet was resuspended in 4 ml of Solution A (50 mM glucose, 10 mM EDTA, 25 mM Tris, pH 8.0) and 4 ml of freshly prepared solution B (0.2 M NaOH, 0.2% SDS) was then added. The solution was gently mixed and kept at room temperature for 5 minutes before adding 4 ml of ice-cold solution C (3M Sodium Acetate, pH 4.7). Tubes were kept on ice for 15 min, and centrifuged at 10,000 rpm for 15 min. After isopropanol precipitation, the DNA pellet was dissolved in 600 µl RNase solution (15 mM Tris HCl pH 8.0, 10 µg/ml RNase A). After 30 minutes at 37°C the DNA solution was extracted with chloroform:isoamylalcohol (24:1) and precipitated from the aqueous phase using isopropanol. The DNA pellet was then rinsed with 70% ethanol, air-dried and dissolved in 30 µl distilled water. In general, DNA prepared by this method was clean and concentrated enough to give good quality results by automatic sequencing (at least 300 bp of sequence). For a few DNA preparations, an additional polyethylene glycol (PEG) precipitation step was necessary, which was performed as follows. The 30 µl of DNA solution were diluted to 64 µl, mixed gently and precipitated using 16 µl 4M NaCl and 80 µl of 13% PEG 8000. After 30 min on ice the tubes were centrifuged at 4°C, the pellet carefully rinsed with 70% ethanol, air-dried and diluted in 20 µl of distilled water.
- [0222] 7. Sizing of inserts. Insert sizes were determined by pulsed-field gel electrophoresis (PFGE) after cleavage with *DraI* (Promega). 100-200 ng of DNA was *DraI*-cleaved in 20 µl total reaction volume, following the manufacturer's recommendations, then loaded onto a 1% agarose gel and migrated using a pulse of 4 s for 15 h at 6.25 V/cm at 10°C on an LKB-Pharmacia CHEF apparatus. Mid-range and low-range PFGE markers (New England Biolabs) were used as size standards. Insert sizes were estimated after ethidium bromide staining of gels.
- [0223] 8. Direct sequencing. For each sequencing reaction 7 µl BAC DNA (300-500ng), 2 µl primer (2 µM), 8 µl reaction mix of the *Taq* DyeDeoxy Terminator cycle sequencing kit (Applied Biosystems) and 3 µl distilled water were used.

[0224] After 26 cycles (96°C for 30 sec; 56°C for 15 sec; 60°C for 4 min) in a thermocycler (MJ-research Inc., Watertown, MA) DNA was precipitated using 70 µl of 70% ethanol/0.5 mM MgCl₂, centrifuged, rinsed with 70% ethanol, dried and dissolved in 2 µl of formamide/EDTA buffer. SP6 and T7 samples of
 5 32 BAC clones were loaded onto 64 lane, 6% polyacrylamide gels and electrophoresis was performed on a Model 373A automatic DNA sequencer (Applied Biosystems) for 12 to 16 hours. The sequences of oligonucleotides used as primers are shown in Table 1.

[0225] 9. **DOP-PCR.** As an alternate procedure we used partially degenerate
 10 oligonucleotides in combination with vector-specific (SP6 or T7) primers to amplify insert ends of BAC clones, following a previously published protocol for P1 clones (Liu et al., 1995). The degenerate primers Deg2, Deg3, Deg4, Deg6 (Table 1) gave the best results for selected amplification of insert termini.

[0226] 15 **Table 1: Primers used for PCRs and sequencing**

[0227] Vector specific Primers for DOP PCR- first amplification step:

[0228] SP6-BAC1: AGT TAG CTC ACT CAT TAG GCA (SEQ ID No. 734)

[0229] T7-BAC1 : GGA TGT GCT GCA AGG CGA TTA (SEQ ID No. 735)

[0230] Vector specific Primers (direct sequencing, nested primer for second PCR step)

[0231] 20 SP6 Mid: AAA CAG CTA TGA CCA TGA TTA CGC CAA (SEQ ID No. 736)

[0232] T7-Belo2: TCC TCT AGA GTC GAC CTG CAG GCA (SEQ ID No. 737)

[0233] Degenerate Primers:

[0234] Deg2: TCT AGA NNN NNN TCC GGC (SEQ ID No. 738)

[0235] Deg3: TCT AGA NNN NNN GGG CCC (SEQ ID No. 739)

[0236] 25 Deg4: CGT TTA AAN NNN NWA GGC CG (SEQ ID No. 740)

[0237] Deg6: GGT ACT AGT NNN NNW TCC GGC (SEQ ID No. 741)

[0238] Primers used for the amplification of *M. bovis* DNA in polymorphic chromosomal region of Rv58:

[0239] Primer 1: ACG ACC TCA TAT TCC GAA TCC C (SEQ ID No. 742)

[0240] 30 Primer 2: GCA TCT GTT GAG TAC GCA CTT CC (SEQ ID No. 743)

[0241] 10. **Screening by pooled PCR.** To identify particular clones in the library which could not be detected by random end-sequencing of the 400 BAC clones, PCR-screening of DNA pools was performed. Primers were designed for regions of the
 35 chromosome where no BAC coverage was [apparent] using cosmid-or H37Rv
apparent

whole genome shotgun sequences. Primers were designed to amplify approximately 400-500 bp. Ninety-six-well plates containing 200 μ l 2YT/12.5 μ g/ml CM per well were inoculated with 5 μ l of -80°C glycerol stock cultures each from the master plates and incubated overnight. The 96 clones of each plate were pooled by taking 20 μ l of culture from each well and this procedure was repeated for 31 plates. Pooled cultures were centrifuged, the pellets were resuspended in sterile water, boiled for 5 minutes, centrifuged and the supernatants kept for PCRs. As an initial screening step, the 31 pools of a total of 2976 BACs, representing about two thirds of the library were tested for the presence of a specific clone using appropriate PCR primers. PCR was performed using 10 μ l of supernatant, 5 μ l of assay buffer (100 mM β -mercaptoethanol, 600 mM Tris HCl (pH 8.8), 20 mM $MgCl_2$, 170 mM $(NH_4)_2SO_4$), 5 μ l of Dimethylsulfoxide (DMSO), 5 μ l of dNTPs (20 mM), 5 μ l of water, 10 μ l primer (2 μ M), 10 μ l inverse primer (2 μ M) and 0.2 units of *Taq* DNA polymerase (Boehringer). 32 cycles of PCR (95°C for 30 s, 55°C for 1 min 30 s, 72°C for 2 min) were performed after an initial denaturation at 95°C for 1 min. An extension step at 72 °C for 5 min finished the PCR. If a pool of 96 clones yielded an appropriate PCR product (Fig. 1A), subpools were made to identify the specific clone. Subpools representative for lane A of a 96 well plate were made by pooling clones 1 to 12 from lane A into a separate tube. Subpools for lanes B to H were made in the same way. In addition, subpools of each of the 12 rows (containing 8 clones each) were made, so that for one 96 well plate, 20 subpools were obtained. PCR with these 20 subpools identified the specific clone (Fig. 1B, lower gel portion). If more than one specific clone was present among the 96 clones of one plate (Fig. 1B, upper gel portion), additional PCR reactions had to be performed with the possible candidates (data not shown).

[0242] 11. **Genomic comparisons.** DNA from the BAC clone Rv58 was digested with the restriction endonucleases *Eco*RI and *Pvu*II, and resolved by agarose gel electrophoresis at low voltage overnight (1.5 V/cm). DNA was transferred via the method of Southern to nitrocellulose membranes (Hybond C extra, Amersham) following standard protocols (Sambrook et al., 1989), then fixed to the membranes at 80°C for 2 hours. The blot was hybridized with ^{32}P labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* type strain (ATCC 19210) or *M. bovis* BCG Pasteur. Hybridization was performed at 37°C overnight in

50% formamide hybridization buffer as previously described (Philipp et al., 1996b). Results were interpreted from the autoradiograms.

[0243] 12. **Computer analysis.** Sequence data from the automated sequencer ABI373A were transferred as binary data to a Digital Alpha 200 station or Sun SparcII station and analysed using TED, a sequence analysis program from the Staden software package (Dear et al., 1991). Proof-read sequences were compared using the BLAST programs (Altschul et al., 1990) to the *M. tuberculosis* H37Rv sequence databases of the Sanger Centre, containing the collected cosmid sequences (TB.dbs) and whole-genome shotgun reads (TB_shotgun_all.dbs) (http://www.sanger.ac.uk/). In addition, local databases containing 1520 cosmid end-sequences and the accumulating BAC end-sequences were used to determine the exact location of end-sequenced BACs on the physical and genetic map. MycDB (Bergh et al., 1994) and public databases (EMBL, Genbank) were also used to compare new sequences, but to a lesser extent. The organization of the open reading frames (ORFs) in the polymorphic region of clone Rv58 was determined using the DIANA software established at the Sanger Centre.

EXAMPLES

[0244] Example 1 : Construction of a pBeloBAC11 library of *M. tuberculosis* H37Rv.

[0245] Partial *Hind*III fragments of H37Rv DNA in the size range of 25 to 180 kb were ligated into pBeloBAC11 and electroporated into strain *E. coli* DH10B. While cloning of fractions I (25 to 75 kb) and II (75 to 120 kb) gave approximately 4×10^4 transformants (white colonies), cloning of fraction III (120 to 180 kb) repeatedly resulted in empty clones. Parallel cloning experiments using partial *Hind*III digests of human DNA resulted in stable inserts for all three fractions (data not shown), suggesting that the maximum size of large inserts in BAC clones is strongly dependent on the source of the DNA. Analysis of the clones for the presence of inserts revealed that 70 % of the clones had an insert of the appropriate size while the remaining 30% of white colonies represented empty or *lacZ'*-mutated clones. Size determination of randomly selected, *Dra*I-cleaved BACs via PFGE showed that the insert sizes ranged for the majority of the clones between 40 kb and 100 kb with an average size of 70 kb. Clones with inserts of appropriate size were designated with "Rv" numbers, recultured and stored at -80°C for further use.

[0246] Example 2 : Direct DNA sequence analysis of BACs.

[0247] To characterize the BAC clones, they were systematically subjected to insert termini sequencing. Two approaches, direct sequencing of BAC DNA and PCR with degenerate oligonucleotide primers (DOP), adapted to the high G+C content of mycobacterial DNA, were used. In a first screening phase, 50 BAC clones designated Rv1 to Rv50 were analysed using both methods in parallel. Except for two clones, where the sequences diverged significantly, the sequences obtained by the two methods only differed in length. Sequences obtained directly were on average about 350 bp long and for 95% of the clones both the SP6 and T7 end-sequences were obtained at the first attempt. Sequences obtained by DOP-PCR were mostly shorter than 300 bp. For 40% of the BACs we obtained only very short amplicons of 50 to 100 base pairs from one end. In two cases the sequence obtained with the DOP-PCR differed from the sequences obtained by direct sequencing, and in these cases *E.coli* or vector sequences were amplified (data not shown). Taking the advantages and disadvantages of both methods into account, we decided to use direct termini sequencing for the systematic determination of the SP6 and T7 end-sequences.

[0248] Example 3 : Representativity of the library.

[0249] After having determined the end-sequences of 400 BACs a certain redundancy was seen. The majority of clones were represented at least 3 to 4 times. Maximum redundancy was seen in the vicinity of the unique *rrn* operon, as 2.5 % of the clones carried identical fragments that bridge the cosmids Y50 and Y130 (Fig. 3, approximate position at 1440 kb). The majority of clones with identical inserts appeared as two variants, corresponding to both possible orientations of the *HindIII* fragment in pBeloBAC11. This suggests that the redundancy was not the result of amplification during library construction, but due to the limited number of possible combinations of partial *HindIII* fragments in the given size-range of 25 to 120 kb. To detect rare BAC clones, a pooled PCR protocol was used. Primers were designed on the basis of the existing cosmid sequences and used to screen 31 pools of 96 BAC clones. When positive PCR products of the correct size were obtained, smaller subpools (of 8 or 12 clones each) of the corresponding pool were subsequently used to identify the corresponding clone (Figs. 1A and 1B). With this approach 20 additional BACs (Rv401-Rv420) were found for the regions where no BACs were found with the initial systematic sequencing approach. The end-sequences of these BACs

(Rv401-420) were determined by direct sequencing, which confirmed the predicted location of the clones on the chromosome. A 97% coverage of the genome of H37Rv with BAC clones was obtained. Only one region of ~ 150 kb was apparently not represented in the BAC library as screening of all pools with several sets of specific primers did not reveal the corresponding clone. This was probably due to the fact that *HindIII* fragments of mycobacterial DNA larger than 110 kb are very difficult to establish in *E. coli* and that a *HindIII* fragment of ~120 kb is present in this region of the chromosome (data not shown).

[0250] **Example 4 : Establishing a BAC map.**

10 [0251] Using all end-sequence and shotgun-sequence data from the H37Rv genome sequencing project, most of the BAC clones could then be localized by sequence comparison on the integrated map of the chromosome of *M. tuberculosis* strain H37Rv (Philipp et al., 1996b) and an ordered physical map of the BAC-clones was established. PCR with primers from the termini sequences of selected BACs were used for chromosomal walking and confirmation of overlapping BACs (data not shown). The correct order of BACs on the map was also confirmed more recently, using 40,000 whole genome shotgun reads established at the Sanger Centre. In addition, pulsed-field gel electrophoresis of *DraI* digests of selected BACs was performed (Fig. 2) in order to see if the approximate fragment size and the presence or absence of *DraI* cleavage sites in the insert were consistent with the location of the BACs on the physical map (Fig. 3). Comparison of the sequence-based BAC-map with the physical and genetic map, established by PFGE and hybridization experiments (Philipp et al., 1996b), showed that the two maps were in good agreement. The positions of 8 genetic markers previously shown on the physical and genetic map were directly confirmed by BAC-end-sequence data (Table 2, Fig. 3). The position of 43 from 47 Y-clones (91%) shown on the physical and genetic map, which were later shotgun sequenced, was confirmed by the BAC end-sequences and shotgun sequence data. Four clones (Y63, Y180, Y251, and Y253) were located to different positions than previously thought and this was found to be due to book keeping errors or to chimeric inserts. Their present approximate location relative to the *oriC* is shown in Figure 3: Y63 at 380 kb, Y63A at 2300 kb, Y180 at 2160 kb, Y251 at 100 kb, and Y253 at 2700 kb. A total of 48 BACs, covering regions of the chromosome, not represented by cosmids were then shotgun sequenced (Cole et al., 1997), and these are squared in Fig. 3. No chimeric BACs

were found, which is consistent with the observations of other research groups for other BAC libraries (Cai et al., 1995; Zimmer et al., 1997). The absence of chimeric BACs was of particular importance for the correct assembly of the *M. tuberculosis* H37Rv sequence. The exact position of the BAC termini sequences
 5 on the chromosome will be available via the world wide web (<http://www.pasteur.fr/MycDB>).

[0252] Table 2 : Identities of genetic markers previously shown on the integrated and genetic map of H37Rv (Phlipp et al., 1996b) [wich]^{which} showed perfect sequence
 10 homology with BAC[ens]^{end}sequences.

Locus	BAC end sequence	Description of genetic marker	Organism	GenBank Accession n°
<i>apa</i>	Rv163SP6	Secreted alanine-proline-rich antigen	<i>M. tuberculosis</i>	X80268
<i>dnaJ, dnaK</i>	Rv164T7	DnaJ hsp	<i>M. leprae</i>	M95576
<i>fop-A</i>	Rv136T7	Fibronectin binding protein	<i>M. tuberculosis</i>	M27016
<i>polA</i>	Rv401T7	DNA polymerase I	<i>M. tuberculosis</i>	L11920
<i>ponA</i>	Rv273T7	Penicillin binding protein	<i>M. leprae</i>	S82044
<i>pslC</i>	Rv103T7	Putative phosphate transport receptor	<i>M. tuberculosis</i>	Z48057
<i>recA</i>	Rv415SP6	Homologous recombination	<i>M. tuberculosis</i>	X58485
<i>wag9</i>	Rv35SP6	35-kDa antigen	<i>M. tuberculosis</i>	M69187

[0253] Example 5 : Repetitive end-sequences.

[0254] Repetitive sequences can seriously confound mapping and sequence
 15 assembly. In the case of the BAC end-sequences, no particular problems with repetitive sequences were observed. Although nine clones with one end in an *IS1081* (Collins et al., 1991) sequence were identified, it was possible to correctly locate their position on the map using the sequence of the second terminus. Moreover, these BACs were used to determine the exact locations of
 20 *IS1081* sequences on the map. Five copies of this insertion sequence, which

harbors a *Hind*III cleavage site, were mapped on the previous physical and genetic map. In contrast, BAC end-sequence data revealed an additional copy of *IS1081* on the *M. tuberculosis* H37Rv chromosome. The additional copy was identified by six clones (Rv27, Rv118, Rv142, Rv160, Rv190, Rv371) which
5 harbored an identical fragment linking Y50 to I364 (Fig. 3, at ~ 1380 kb). This copy of *IS1081* was not found by previous hybridization experiments probably because it is located near another copy of *IS1081*, localized on the same *Dra*I fragment Z7 and *Asn*I fragment U (Fig. 3, at ~ 1140 kb). Furthermore, the position of a copy of *IS1081* previously shown in *Dra*I fragment Y1 (Fig. 3, at
10 ~ 1840 kb) had to be changed to the region of Y349 (Fig. 3, at ~ 3340 kb) according to the end-sequences of BAC Rv223. The positions of the four other *IS1081* copies were confirmed by the sequence data and therefore remained unchanged. In total 6 copies of *IS1081* were identified in the H37Rv genome in agreement with the findings of others (Collins et al., 1991).

15 [0255] In addition, a sequence of 1165 bp in length containing a *Hind*III site was found in two copies in the genome of H37Rv in different regions. The end-sequences of BAC clones Rv48 and Rv374, covering cosmid Y164, as well as Rv419 and Rv45, that cover cosmid Y92, had perfect identity with the corresponding parts of this 1165 bp sequence (Fig. 3, at ~ 3480 kb and ~ 900 kb).
20 Analysis of the sequence did not reveal any homology with insertion sequences or other repetitive elements. However, as each of the two locations showed appropriate BAC coverage, chimerism of the sequenced cosmids Y164 and Y92 can be ruled out as the probable cause.

[0256] Example 6 : Using BAC clones in comparative genomics.

25 [0257] The minimal overlapping set of BAC clones represents a powerful tool for comparative genomics. For example, with each BAC clone containing on average an insert of 70 kb, it should be possible to cover a 1Mb section of the chromosome with 15 BAC clones. Restriction digests of overlapping clones can then be blotted to membranes, and probed with radiolabelled total genomic DNA
30 from, for example, *M. bovis* BCG Pasteur. Restriction fragments that fail to hybridize with the *M. bovis* BCG Pasteur DNA must be absent from its genome, hence identifying polymorphic regions between *M. bovis* BCG Pasteur and *M. tuberculosis* H37Rv. The results of such an analysis with clone Rv58 (Fig. 3, at ~1680 kb) are shown here. This clone covers a previously described polymorphic
35 genomic region between *M. tuberculosis* and *M. bovis* BCG strains (Philipp et

al., 1996a). *EcoRI* and *PvuII* digests from clone Rv58, fixed on nitrocellulose membranes, were hybridized with ^{32}P -labelled total genomic DNA from *M. tuberculosis* H37Rv, *M. bovis* (ATCC 19120), and *M. bovis* BCG Pasteur. Figures 4A and 4B present the results of this analysis, where it is clear that several restriction fragments from clone Rv58 failed to hybridize with genomic DNA from either *M. bovis* or *M. bovis* BCG Pasteur. On the basis of the various missing restriction fragments, a restriction map of the polymorphic region was established and compared to the H37Rv sequence data. The localization of the polymorphism could therefore be estimated, and appropriate oligonucleotide primers (Table 1) were selected for the amplification and sequencing of the corresponding region in *M. bovis*. The alignment of *M. bovis* and *M. tuberculosis* H37Rv sequences showed that 12,732 bp were absent from the chromosomal region of the *M. bovis* type strain and *M. bovis* BCG Pasteur strain. The G+C content of the polymorphic region is 62.3 mol%, which is the same as the average genome G+C content of the *M. tuberculosis* genome, hence indicating that this region is not a prophage or other such insertion. Subsequent PCR studies revealed that this segment was also absent from the Danish, Russian, and Glaxo substrains of *M. bovis* BCG, suggesting that this polymorphism can be used to distinguish *M. bovis* from *M. tuberculosis*. Analysis of this sequence showed that 11 putative open reading frames (ORFs) are present in *M. tuberculosis*, corresponding to ORFs MTCY277.28 to MTCY277.38 / accession number Z79701 -EMBL Nucleotide Sequence Data Library (Fig. 5). FASTA searches against the protein and nucleic acid databases revealed that the genes of this region may be involved in polysaccharide biosynthesis. Among these putative genes, the highest score was seen with ORF 6 (MTCY277.33), whose putative product shows a 51.9% identity with GDP-D-Mannose dehydratase from *Pseudomonas aeruginosa* (accession number U18320 - EMBL Nucleotide Sequence Data Library) in a 320 amino acid overlap. The novel *M. bovis* sequence of the polymorphic region was deposited under accession number AJ003103 in the EMBL Nucleotide Sequence Data Library.

[0258] As it appears from the teachings of the specification, the invention is not limited in scope to one or several of the above detailed embodiments; the present invention also embraces all the alternatives that can be performed by one skilled in the same technical field, without deviating from the subject or from the scope of the instant invention.

Table 3 : End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the I-1945 *M. tuberculosis* H37Rv genomic DNA library.

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

Clone Rv101

.....Rv101SP6.seq:.....
AATACTCAAGCTTGGCCAGCCGTCGATGACAAGAAATATGTCCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTG
GCGGTACCGCGCCACCGATTCTATGCCGTGGTCGCGGAAAAATGCCTCCCGAAATCGCACGGCCGACTCCAGTTCCGGC
GAGCATCCGCGATGCCAGCTGCGGCTGCGCCCTGCCGGCCACGGCACCCACATGCGGCAGTTCTGTCACCTGGGCCAG
CGCCCCGCCCGCAATTCCAAACAATAGAACTGCACCCGGCCCGCATCGTGGGTAACAGCCAACGCCATGATCAGCGT
CCGCAGCGCGTTGACTTGCCCGTTTGCGGTGACCTACGAACGCGACATTGCCTGCGGCCCGGACAAGTCGATCGT
GCGCGGCACCCGTGACTGCTCTAACGGGCGATTGAAATTCGCGAT (SEQ ID NO.6)

.....Rv101T7.seq:.....
CCACCCGTGTAATTTGGGATGGGCAAAAAGGCGAAGCACCAGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG
TTAGGGCTTCTCGCGGAAGGCCCGAACGTACGGCGTTTCAACACCTCGCGTCGCCCTCCGACCGCGAACATTCCGGGG
ATGGCAGCAACCTGCTGGCACCCTGGCCGGGCGATGATCTGCAGCGTCGCCCGGGGTAGTCGCCCGCCGGGCGGCTAC
ACTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCCGACGCAACGGTTCCTACACCGCGATATGTTGCGCT
CGCTGCCCGGGTGGACCGGT (SEQ ID NO.7)

Clone Rv102

.....Rv102SP6.seq:.....
AATACTCAAGCTTTCGCCGATACCCGCCATGTCGCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGGGG
ATCCCAAAGTGCGGATGATCGGGCCGCTACGTCGTGGTGTACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTC
GGTCCACGCGGTGCGGCACATGGTGGACACCACACCGCCACCGCACGGGGTGAAGGCCTATGTCACCGGTCCGGCAGC
ACTCAATGCCGACCAGGCCGAGGGCGGAGACAAAAGTATCGCTAAGGTACCGCGATACCAACATGGTGATCGCAGC
AATGTTGCTAGTGATCTATCGCTCCGTAATTACCGCGTTCT (SEQ ID NO.8)

.....Rv102T7.seq:.....
GTGCCGTTCCAACCCGAATTGGCTTTCGGCGCCATCGGTGAGGACGGCGTGGGGTGCTCAACGACGACGTCGTCCGC
GGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGC
TTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATACGGCATCGCCACCGGAGCG
ACGGCCAAGGCGGCGTGCCAGGTGCCCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCAGAC
GACATCGTGCGGAGATTCGCCGGGTACGCCGATGAGGTGGT (SEQ ID NO.9)

Clone Rv103

.....Rv103SP6.seq:.....
AATACTCAAGCTTTCGGCGGAAACGGACACATTGCGAATATTGATGACAAAATAAAAAATCATTGATGGTTTGAGTCAC
CAGGCCGATCAAGCCTTCGCCGAGCCAAATTTCAATCAAGAGGCCAAGCCCGTACCAATCAGCCCCGCAACGAGGGA
TTCCGTCATTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAAACGGTCGCCGTTG
CACGACATTAAATGTCACGGTATTGTAGATTAAAAAGATACCCAC (SEQ ID NO.10)

.....Rv103T7.seq:.....
TGCTCCCGAAACCTGGGGGTGTGCTGCTGTATGCACGGCATAACGGACATCCTTCCCCTGAGACCCGCGGTGCAAC
CAGCCACGTGTCCATCATAGNGGGTCAACCCCGGCCAAGGGCGACGGCACGCCAAGTTCCGCCACCGTTAACCTAGTG
CTGTTAGCTTCATTTGCTGCGATCAAAACAGCTGGTCCGGCGTTAGGAAGTGAATTGAACTCAACCGATTGGTGCC
GCCGTAGGTGTCCTGGCTGCGGTTGCGCTGGTGTGTCGCGGTGTGGTAACGACGACAATGTGACCGGGGGAGGTGCA
ACCACTGGCCAGGCGTCCGCAAGGTGATTGCGGGGGGAAGAAGACACTCAAAGCCAGTGGGT (SEQ ID NO.11)

Clone Rv104

.....Rv104SP6.seq:.....
ATACTCAAGCTTTGCCGACGAGCGGGCGATGTTGATGACGGGAAACCCAGCGCACAAACCGACGATTTTGGCGTAGCC
GGCGGACGTCTGCTCGATTCCGATCACGTGCGCGCTCGCATCGAGCATGGCGCCGGCGACGGCTAGCAGCGATCCGCC
GTCGTCGAGGAGCACGACACGAGCCGTACGCCGGCCGTAAGCCGCGCCAGGATTGGCGGAAAAACCGTTCTACGTG
GCGGGTGTACTGGGTGTCGAATGATTCGTGGGGTGCGTAGGCGTCGCTGCAATCGTCGACATAGATGCCGTGCGGGCCG
CATCGCGTCGACAACCTCCGGGTGAGTGGAATAGCACTTGCCGATCACCGCGACGTTGCGCGGATGAGGCCGAACCCGA
ATA (SEQ ID NO. 12)

.....Rv104T7.seq:.....
TCCTATGTCCCTGCCGAGCANGTATCGAACGCGGTGACAGATTTGTCTATCCTGGACCTGACGGTGAGGTGGAAGTT
TTCCAGGAATTCCGGCAAATCGGTAAGAGCCTGAAGAATTCCGTATCGCCGGACGAAATCTGCGACGCATACGGGGGC
ATATACGCTTCGGGTTTACGAGATGTCGATGGGGCCGCTGGAGGCTTCACGTCCATGGGCCACAAAGGATGTTGTGCG
CGCGTACCGTTTTCTGCAGCGGGTGTGGCGCTTGGTCG (SEQ ID NO. 13)

Clone Rv105

.....Rv105SP6.seq:.....
ATACTCAAGCTTGATTCCGCCGAAACCGACCGTGAGCACCCCGCCAGCCACCACGCTCGGGTGGGGGCGGGGCCCGG
GCCGCCAGGTGCTCCGCTCGGTGATGGCAGCCACCGCGACACCACCGGCTGCGCTACGTCTAACCATTCAGGGC
GAGCTACATCAGCTCGGCCGCCAGTGTTGCGGCCCTCTTTCCAGGTGGAAGTCTATACCGATATGCGCATCCGCAGC
CGCCACCTTGAGAACAGACGATGCCCTACTAATGCTTGTCTGGCGGGGC (SEQ ID NO. 14)

.....Rv105T7.seq:.....
GGTACGCTTCGGTCGAGTCTGCGAGTATGTCATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCGCCACACCT
TCAGTTGCTCACCAGGAATCCAACCGGTAGAAGTTCGGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGAC
GGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTCGGGGTGGTCGCGACGCGCATGGGGCCACCATCGCAT
TCACCAGGTCTGCGCGAATCACCAGCACGTAGACGGTTCCTTTCTAAGCAACACCGAAGTTTCAGGACCCGAATGCT
CCGGGAAACATGTACGGTAGGTGCGTATTCGGCTACCGGCTGA (SEQ ID NO. 15)

Clone Rv106

.....Rv106SP6.seq:.....
GGCGTCAACGGTGTGCGAACCCGCGTCAAGCAATTGGTAGGCCTGCAGTCTGTGAATCAGGCCGACGCTGTGGCCGCC
GCGGC (SEQ ID NO. 16)

.....Rv106T7.seq:.....
GGCTNGCGTACCCGGTACCGGCCGCGGGCCTACCACGTGCCGGAAGTGAAGCGCAGTAAGCCCTCAACGCGCCACCG
CTTTGGCCCGCGCGCCCGGCGTAGGCGCATCGGCGGTGGCCGTGGGGCGGCGCACTGCGACCTCACCAGCGGCTTTCCG
AGCTTTGTCGATCAACCGGCCAGCATGGTCGANGATGCATTGCGAGACCATATTCGAAATTGGTTTCATCGGGGGCCC
CGATCCGATGCCCCCTCCAGTTGCGTGAGCAANACGGAGTTCNTCGCGGGATCGATGGCCACGGGGTGTTCATGG
CGGATGGTCCGCTGCCCGCGCACTGGCTCTTGCGGGAGAACCAGTCTAGCACCAACCGATCCGCGCACGTNG
(SEQ ID NO. 17)

Clone Rv107

.....Rv107T7D4.seq:.....
CGTAATNTCGCGCACANCCANGACTTCTGGGGGATCNGCTGACAGTGGTNGGATCCCAAATTGCGGATGATCGGGCC
GCCNACGTCGTTGTGTACCTCNTCNGTCACAACNAANCCGAANCATGACTCGGTCCACGCGGTGCGGCACATGGTG
GACACCACACCGCCACCGCNCGGGGTGAAGGCCTATGTACCGGTCCGGCAACACTCAATGCCGACCAAGGCCGANGCC
GGACACNANAGTATCNCTAACGTACCCGCGATCACGAGCATGGTGATCGNNCAATGTTNCTANTGATCTATCGCTCCG
TAATTACCGCGGTTCTCGTCTTGATCATGGTCGCANCGAACTCCGGCGCAATCCGCGGATTTCATCGNCTTGCTCGCGG
ATCAGATATTTTCAGCCTTTCACATTGCAACNAACCTGCTCGTCTCATGGNGATGCGGCGACACGGACTACCGATATC
ATGCTCGCCGTTACACAATCNCGCCACGCCGCGGAAGACNGGAAACGCTTCTACACAATNTTNCGGGACGCCACTNAA
CTTGGTTCNGGTTTGACATTGCCGCGCATGNTGCCAGCTTTCGCGGCTCCCTTA (SEQ ID NO. 18)

Clone Rv108

.....Rv108T7D4.seq:.....
TGAATTTCCCGATCCCAATCTCGGTTTCAGATACAGGTGCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGC
CCTGCGNCTGCAGCANACCATCGACGCCATCGAATTGCCGGCAATCTCGTTCAGCCAATCCATACCCATCGACATTC
GCCGATCGACATCCCGGCTTCNCCCTTTAACGG (SEQ ID NO. 19)

Clone Rv109

.....Rv109SP6.seq.....
AACAGCTATGACCATGNTTACGCCAAGCTATTTAGGTAACACTATANAATACTCAAGCTTTTACGGTGATCGCGCATC
ACCTGGTTTCATGAACTGGAAGCAGCGCANCCTTCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCCGCGGTCTCNGG
TGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACNAACNACNCC
AGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCCGGTGTGGGGTGT
TTCGGCGACCGGCAGCCAGGTGGTCCACACTGCCGACGGGCGCCGCGAGCCGTTACCGACCAAGCCGCCGAACAAGT
CCGCCGATCGCATACTCCAACCGGTTGCGGTACTGCAGGTGAGCTGGCGTACCTCCTCNCGCTCGGCCAAGTCT
TGCTCCANCACGTGCGAGAACGGCAAGGAACACGTTCA (SEQ ID NO. 20)

.....Rv109T7.seq.....
GACCGNCCATGTTCCACAATGTGGTGCCAGTNCGGNGGCTACGTGCCATCNANACACTGGCGCAGGCTATCGCACC
CGTTATCNGCTACGAACAAATCNCGGTATGCGTTCTTTTANCATGAGTCGGCGACCGNCGATCATGGTCGACACCCACG
ACNGAAATACGAGATCGCCNTCNAGCNTGTGTGCCGCGGATTATCANGACTGACCTCCTGGCTGACCGGNNTGTNTG
GTCCGGATGCTTGGCGCCCGCGCGGTGNTCGTGGTTCGGCTCGGATAGCGAAGTCAGCTAATTCTCGTGGCAGCTCG
AAAGGGTCTGCCGGTGCCGGTCTTTGCGCAAACCATGCNCATGTTACGGTCCCTCGGGTGGCGCCTGGCGGCGGC
(SEQ ID NO. 21)

Clone Rv10

.....Rv10SP6D2.seq.....
GGGATGGGCGGGCCCGCTAAACTCTTCGTGTTCCACTAACTCCGGGAGGGNCAATCTCGGGCCGTTATGGCTCACGTC
GCGTCGCCCTCCGACCGCGAACATTCGGAGTTGGCAGCAACCTGGTAGCACCTGGCCGG (SEQ ID NO. 22)

.....Rv10T7D4.seq.....
NCCGTGCTTGACAAGTAAATATGTCGCAAAAGTCTCAGCGGCCGACTTTGCTCGCAGGTGGCGGTACCGGCCACCG
AGTCGATGCCGTGGTTCGCGGAAGAATGCCTCCCGAAATCGCACGGCCTTCCCNNTTAAACGGA (SEQ ID NO. 23)

Clone Rv110

.....Rv110SP6.seq.....
TTTAGGTGACACTATAGAATACTCAAGCTTTTGGTCTAGCCGGCCGAGCAGCAGATACGGGTGTCATTGGCCACCGGCGG
CGGCTGTCCGGGAAATGGCGGGTCCCGGTGGTTTTGCTGATGAGTGCTGAACCGTANTCGAAGTGGCGCGCTCAGA
CTCCACCCANCCAGCAGGCAGCGCGAAGCTGAATCCTCCAACCGGGTTGTCNATCCGGACAAGTTGGGGTGCCTTTGG
GGCAATGACAGGTGGCNGCGGTGCGTTCGGGTCCGCCGGCGGAAGTGCTGCGTTGGGATCNCCTGCTGGGCATTCCGGC
NTTTTGGCGCGCGCGGTGGTNGGGGGCAACAGGTNTCCNGTGCGGGTGGCGCTCAACGGTCNACGGCGCAAGCCG
CCGTTGTTGTTACNNGGGCGCTGGCTCCGGATCGCGTTGGCGGTTCNCCG (SEQ ID NO. 24)

.....Rv110T7.seq.....
CTACACCATCGAATACGACGGGTGCGCNACTTTCCGGGTACCCGCTCAACTTTGTGTCGACCCTCAACGCCATTGC
CGGCACCTACTACGTGCACTCCAATACTTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATAC
GGTCGGTCCCACGATGACCCAGTACTACATCATTCGCACGGANAACCTGCCGTGCTAGAGCCACTGCGATCGGTGCC
GATCGTGGGAACCCACTGGCGAACCTGGTTCAACCAAATTTGAANGTATTGTTAACTGGGCTACNCGACCCGGC
CTATGGTTATTTCNACCTCNCGCCCAATGTTGCGACTCCGTTTCGGGTGTTCCANAAGTCNCCCGGTGCTCATCGC
CGAANCTCTCNCCTCCCGGACCCACAGGGAATCNGCNATTTNCCTACAAATCANCCACCTCCA (SEQ ID NO. 25)

Clone Rv111

.....Rv111T7.seq.....
GCATGATCGGCCACCTTTCGGGCCCGCCGCATACGGCGGGTACCGATCTCCGCGTCATACACCCGCGGGTAATCGC
CGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACTCTGATTGAATCGAGTTCAGGTCCAGCGGGTGGCGCACCAACG
GCGCGAGCTCAACGACGTCAATCNCGTTGTCGTTTCTACGGTACCCGACCCTGGTGACCGTAGTTCNCCG
(SEQ ID NO. 26)

Clone Rv112

.....Rv112SP6.seq.....
GACACTATAGAATACTCAAGCTTGCCAACCGCCAGCCTGCATCCGGCGCGGANCACTGCTCCGCCGACCAAGTACGAAC
CAACCTGCGGTGCCCCAGGCCATTGACGATGTGCTGGTTCGGCGCCCGAGTCCGCGCACCATCAACGCCGCGGGCACC
ACCANGGCGGCCCCACCTGACGGCGACGATCATTCGGCGCCCGCTACGGCGGGCGGGGCTCGAACANGCACAGCA
TCAACGTNGTCAACCGGCCGTGACCGGCCCGCATCGTCACACCACCAAGCCCATTTGCCGTCTCTCAACNNGGGCGA
CCCGGCCCGCATCGTCACCGNCTAAGGCCATTGCCGTCTCTCT (SEQ ID NO. 27)

.....Rv112T7.seq.....

TCGGCGCCATCGGCACCTTCGAGGACCTGTATTTCGACGCCGTGGCCNACCTGAGG
CCCGGTTGATTGCTCGCTCGGCCTTGGCGGATGCCACCCNGCGCCTGGTGGTTCGATCCGC.
NGCTTCTGCTGCTGCGACACCCACNACGTGGTGGCACCAGCTTTAGCTGGCAT
CNACTCCAGACNTTCCACNAANGGTGCGCCNCCCAATGTNCCGNANTGTCTCCGGNTCC.
GNTTCCACNNGGTTACGGGCCCCNTNCCGGCGGTCTNCCCTCCCAANTACCAATACGCC.

Clone Rv113

:Rv113SP6.seq: (SEQ ID NO. 29)

ATACTCAAGCTTTATGGTATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTC
ACATGAGCCAGCCTCTCGTGGCGGTGCGGTGCAGGTGCTCGGGCAGCTCGGCCGCGAACAGCCCG
AAAACCGCTTTTCATATCCCGGACGAAAGAGCCAGTTCGGCTACTTAACCCCTCCGGAACCG
CAGCGCTTCTCCACCAACCGGGCCCGGTGT
:Rv113T7.seq: (SEQ ID NO. 30)
TCGGCTCAGGCCGCGCTGCTGGTAGAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGT
GCCATCGAGACACTGGCGCAGGTATCGCACCCGTTATCGGCTACGAAGCAATCGCGGTATGCGTTCCTGAGCATGA
GTGCGGCGACCTGCTGATGGTCGACACCCACGCGAAAGACGAGATCGCGCTCAAGCATGTGTGCCCCGCGATTATC
AGGACTGACCTCCTGGCTGACCGCATGTTGGTTCGCGATGCCCTGGCGCCCGCGCGGTGGTCTGGTCTGGTCTCGGA
TAGCGAGGTGAGCAATTCTCGTGGCAGCTCGAAAGGGTCTGCGGTGCGCGGTCTTTCGCAACAATAGCGCAGGT
TACGGTTCGCGGGGTGCGGCTGCGCGCGGC (SEQ ID NO. 31)

Clone Rv114

:Rv114SP6.seq: (SEQ ID NO. 32)

CAAGCTATTAGGTGACACTATAGAATACTCAAGCTTCGCGTCTACGCCGCGGAGCATCCGCAAGCGCTCAGCA
GCGCGTTCCGTAGANCTCAAGCAGGTGGCGCAATGACCGAAACCCAGCCCGCAAAACCCCGCGGCCCGCGG
GGCGCCGCAATCGTTCGTGTTGGAGCGGCCCATCCANACCGTTGGGCGCGCTAAGGANGCCGTGGTACGAATGCGG
CTGGTCCCCGCGCACCGCAAGTTCGACCTCAACGCGCGCAGCTTGGANGACTACTTCCCAACAAGGTGCACGAGCAG
TTGATCAAGGACCCCTGGTCAACCGTGGATCGGTTGAAAGTTTCGACATCTTTGCCACCTGGCGCGCGCGGT
CCGGTCAGGCCGGGCTGCGCTGGGTATCGCCCGGCATTGATTCTGGTATCCCCNGAAGAACCG (SEQ ID NO. 33)

:Rv114T7.seq: (SEQ ID NO. 34)

CGGTGGCCACCGCTTCTGCGGTGCGCGCGCTCGACAATGACCGTGTCTGCTGACCACCGCGTTCGGGCC
GAGCCAGCACCTTCAAGCCACCTCGCGCAGCACCATGCCGCGCTCGGGGTTGACCACCTGGCCACCCGTCACCACC
GCCAGGTCTCAAGGAAACGCTTACGGCGGTCAACGAGTACGCGCCCTTACCGCAGCATAGTGGCTTACCGTTCC
AATCGCGTTGACGACCGCTCGCCCAACGCTTCGCCCTCCACGTCTTCAGCCACGATAGTGGCTTACCGTTCC
TGCAACCTTTTCAGCAATGGCAACAGATCGGGAAGCGANCTGATCTTGTCTTGGTGCN (SEQ ID NO. 35)

Clone Rv115

:Rv115SP6.seq: (SEQ ID NO. 36)

CCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTTGGCTGGGTGCGCTTCGAATTTCNGCGTGCACCGCTATGG
GTTGCANAGCGGCTGGCGCCGACACCCACTGGCCCGGTGTTTCGCCCCGAACCCGGATCATGGTGAGCGAAAA
GGANATTNCCTGTTGATGCTGGGATTCGCCACGCCAAGGCATCTANCGATTACTCTCCNCGGGTGGGAAAAAGTGC
CCAATCCCCCTCCCTCAACTTTCNAACAATCATTCGGTTTCNCCNTCCGGTTGGNGGTAACNNCCAATAAAACC
CCTGCCCG (SEQ ID NO. 37)

:Rv115T7.seq: (SEQ ID NO. 38)

GCCCGCNCATGGCCAATCCCCAAGACATCATTTGGCCAGTGGCCGGGCGCTAACAGGTTCCAGCCCCCACCANTGCC
GCTCGAACATGCGGTGCAACCCATTTCGAGGCGCGGAAAGCACCCGCGAAGCGGCTGCAAGTTCGCGG
CCCAATAATGTCGTCGCAACCCATTTCGAGGCGCGGAAAGCACCCGCGGAGCGCGTGGTGCATGCC
GCTNTCAGCGCGCCACATGGGGTGGCAATCGGCACGGCAGGTATGCCGCGCGCAACCCGAGCGGTGGTGCATGCC
ACGGTCCGCGANGCGCANACCCGCAATGCCGAANCCACGAAACATCGGGCGCATCCACCTTCAACC (SEQ ID NO. 39)

Clone Rv116

:Rv116SP6.seq: (SEQ ID NO. 40)

ATACTCAAGCTTGGCCAGCGCTGATGACAAGAAATATGTCGCGAAAGACTCAGCGGCGGACTTTGCTCGCAGCTGG
CGGTACCGCGCCACCGAGTGCATGCCGTGGTTCGCGGAAGAAATTCGCAAGGCAATTCATTCGGGA
AGCATCCGCAATGCCAGTGGGTTGCCCTGCCGCGCACCCACTTGGCGGATTGGCTCCACCTGGGCCAGC
GCCCGCGCCAAATTCAAACAATAAAATTGCACCCGCG (SEQ ID NO. 41)

.....Rv116T7.seq:.....
CCACCCGTGTATTTTGGGATGGGCAAAAAGGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG
CTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTCTGGGG
ATGGCAGCAACCTGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTCGCCCGGGGTAGTCGCCGCCCGGGCGGCTAC
AGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCTACACGGCGATATGTTGCGCTC
CCTGCCCCGT (SEQ ID NO. 36)

Clone Rv117

.....Rv117SP6D2.seq:.....
CTGCCCATGTTTGGGGACGCCGACCAGCCGATGCTGGAGGCCTACACGGCCCTTGGTGCCTGGCCACGGCGACCGA
GCGGCTGCAACTGGGCGCGTTGGTGACCGCAATACCTACCGCAGCCNGACCCCTNTCNCAANAGGATNTTGTTCGCC
GGACCCCNCTC (SEQ ID NO. 37)

.....Rv117T7D4.seq:.....

CCGACTTTCGCGGTACCCGCTCACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCA
ACTTCATCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACT
ACATCATTCGCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAAC
TGTTCAACCAAACTTGAAGGTGATTGTTAACCTGGGCTACGCGACCGCCTTT (SEQ ID NO. 38)

Clone Rv118

.....Rv118SP6.seq:.....

ATACTCAAGCTTTGTACACCAAGTGTTCGACAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT
CGCCACCACGCTGGTCAGTGCGCGTTAGCTCGCTTGCGGCGCTGCAGCAGCCATTCCGGGAAATACCTGCCCTGGCG
CAGCTGGGGGATCCCAACTTCAATGGTTGCGGCACGGGTGTCAAATTCACGGTGGCGGTAGCCGTTGCCCTAATTGGA
CCGCTCATCGCTGCTTTGCGGGTACCCCGCCCCGCACAGGGCTTCGGCTTCAGCCCCCATCAGGGCGGCAATAAACTT
CAAGAGCACC (SEQ ID NO. 39)

.....Rv118T7.seq:.....

GAGGCAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACGGATCTGACCGAAGTCGCTGCGGTGCAGCC
CACCTCATTTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTCCGCTTGCCGACGGCGACGCGGTAGGTGG
TCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCGACGCTGGTTCGCGGTTGCGCCGCGAAAGCGGCGGGTCGG
GTGCCATCAGGAATGCCTCACCGCCGCGGCACTGCACGGCCAGTGCCGCGGCGATGTCAGCCATCGGGACATCATGCT
CGCGTTCATACTCCTCGACCAAGTCGGCGGAACAGCTCGATTCCCGGACCGCCAGCGCATTTGGTGATGGAATCGGCGA
ACTTGGCCACCCGCTGGGTGTTGACATCCTCGACGGTGGGCAATTGCGCCTCGGTAAGCTTTGCCGCGTAGCCTTTTC
ATC (SEQ ID NO. 40)

Clone Rv119

.....Rv119SP6.seq:.....

ATACTCAAGCTTCACTGACAAGGGACGAATTTCGTGGCCCGCTGTTGACTGGGTGGTGGCCGAGCTGGTCGCCACCA
CTCAGGCCGCGGTACGGCGGTACCGGCGCGGGAGCAAACTCGCGCGGCATGGCCAACTTCTTGGGACCATCACCG
CAGACGCCCCGCTTCGGACCCCTGCTGTCCACCACACAGTTGGCCAACGCATTAATCACCCGCAAGCTTGGCGAATCCA
CCGCCCTGTTGCG (SEQ ID NO. 41)

.....Rv119T7.seq:.....

TCCATCACCCGATGTGGCNGGAGCACTGCCATGTGATCTCAACTACCACCTCCGGCCGTGGCGGTTGCGCGCCCCGG
GGGGTCCGCGGAACTCGACGAGGCGGTTCGGAGAAATCGCCANCACCCCGCTGAACCGCGACACCCGCTGTGGGAGA
TGACTTCGTTGAGGGGCTTGCCAACCACCGGATCGCGGTGGTTGCCAAAATTACCATGCGTTGGCTGACGGTGTG
CCTCGGCAAAACATGATGGCACGGGGGATGGATCTGCCGCGGGACCGGAGGTGCGCCGCTATGTGCTGACCCCGCTC
CTACCAAGCGGCA (SEQ ID NO. 42)

Clone Rv11

.....Rv11SP6.seq:.....

AGCTTTGCAGTTGCTGAGTAATGTGCGCCAACGTCAACACAACCGCGATGAATTCAATCATGCCGCCAGGGCGGCCA
ACCCAATGGTGGCCGCGAGCGGACGCTCGATCGCAGCGGAGGTTGCCGCGGCCAGTTGATTACGAACAGGGTGA
GGTCATAGGCGGGCAGGATAGTGACGAAGGCAAGACCTCCATCTGCCGTGCGGAAGAAGTATCGAG

(SEQ ID NO. 43)

.....Rv11T7.seq:.....
AGCTTCAGAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGC GGCCCGCACCG
CCGGCATCTCCCGGTACGCAGGGCCGCGGCCCGCGCGCAGCGACGGCGTGTTCGCGCAGTTCCCGTCAATGATGC
TGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCGTGCGCTTCTACTAATCGCGGTGCTCAGCAGCGTCTCGACAGCCA
CCACCCGAGTGGCGACCAGCTGCTCCACCACGGACCGCAGCGATGCCCGTC (SEQ ID NO. 44)

Clone Rv120

.....Rv120SP6.seq:.....
ATACTCAAGCTTCAGTTCCCTCCACGACGCGTTCCCAAATGAATTTCCCGATCCCAATCTCGGTTCAAGTACAGGTC
GCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGCCCTGCCGCTGCACCAAACCATCAACGCCCTCAAATTGCCG
GCAATCTCGTTCAAGCAATCCAT (SEQ ID NO. 45)

.....Rv120T7.seq:.....
GCTCTACGCCGCTACGGGTCAACATGCATCCCGAGCAGATGCTCGAGCGCGCACCCCACTCGCCGATGGCCGGAAC
CGGCTGCTTACCCGGGTGGCGGCTGACGTTCCGGCGGCGAGGACATCNGCTGGGAAGGGGCGCTTGCCACCGTCGTCTNA
AGACCCAAATTCGAAGGTGTTCTGTCGTGCTCTACGACATGACCCCGGCGGACGAGAAGAACCTTGACCGGTGGGAAGG
CTCCGAGTTCGGTATCCACCAGAAGATCCGATGCCGCGTGGAGCGCATTTCTCGGACACCACAACGGGATCCCGTCC
TCG (SEQ ID NO. 46)

Clone Rv121

.....Rv121SP6.seq:.....
ATACTCAAGCTTGCCAAAGAGACCTCGTCCACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCGGCTTGGCGTCGAC
CCGCGTAAGGCAAACAGATGGTTCGCGGCACGGTCAACCTGCCACACCGGCACTGGTTAAGAACTGCCCGCGTCGC
GGTTTTCGCGGTTGGTGAAAAGGCCAATGCCTGCGTTGCCGTTGGGGGCGGATGTTGTGCGGAGTGACAATCTGATCA
AAAGGATTCAGGGCGGTTGGCTGGAATTCATGCCGCAATCGCGACACCGG (SEQ ID NO. 47)

.....Rv121T7.seq:.....
CCACGCGTGGATCAAGGTACCGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTGCGCGTTAGCGC
CGGATTCCACCACATCCCTTGCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCCATCGAGATAGTGAGCA
ACGCAATCCGTGCGGTACGGTTCGGGTGCTACTCGATGTGCGCGACCTTGCGGTTGACACCATCTTTGTCAATTGCGGC
GAAAGTCGATCATCCGTAAGCGCGCTTATGACCGCGCCTTTGTGCCGGTGGTAATCCGGCCATGCGCGTTGCGTC
CACCGCGACGTGCAGCGGGCGCACACGCACTTCTCCGGGTTGACCGGGTNATCTC (SEQ ID NO. 48)

Clone Rv122

.....Rv122SP6D2.seq:.....
GCAGCATGACGGCGGTAGCGAACACCGCCGGATGCAGCGCAAGTAGCGTCGATGTGCTCAGGAATCGCCCCGGCACC
GCGATCTCGANGATCACCAGTGCCACCCCTGCAGCGCNACACCGACGATTCGTTACACCGCCACGGCGATCAGGCCC
TGGGCCATCTGATTGGAGCTGGCGTANATGGCGGCGATGGTGACGATGGCCAGCGCCACATACATTGTGCGCGCCAGA
ACCACGGCGTTGGGGCGGGGTCGATGAACACTAGGCGACGAGATCGCCCGGGGTCAACAGGTTGACCATCAGAAAG
CCTGCGACTAGCACGGCGGCGCCACTAGGAAGTACAAGAANGTGGCCACCACCCATGCAGGATCGGGGTAAAGGCTGA
TGGTCCCGAAATCGACTCCGGCCTAATACATGACTCTCTCCTTTGCGTCATCGCCTTACTTGTGCGCGGAA
(SEQ ID NO. 49)

Clone Rv

.....Rv123SP6D2.seq:.....
GGGACACACCTCGATGCTGCCGCNATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGC
TTCCGCCGCGGGCGTGACGCATCCCGTTGACCGGCCGGANCTCTCTA (SEQ ID NO. 50)

.....Rv123T7D4.seq:.....
TGGGCGCCTCTTTCGGCCTTCCCNNTTAAACGNAGCANGACATTCTGGGTATCGAGTTGTAAGTGGTGGTGGCG
ATGTGCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCGGGTTGAAAGAGGAAATTGGG
GCCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGGAGTGGTGACGCTGCCGGCATGGTGTTCGCC
GTTACCATGTGCTTGTGTTGTGTTGAGCGATTTGCGAATTATTGGTCAGATCGGTACCAACATCGCCTTCCC
(SEQ ID NO. 51)

Clone Rv124

.....Rv124SP6D2.seq:.....
CCGATCGGCGCCGCANCTGGTTGGTGTNCGGATGAATCCGCAGCGAAAATGTAGCTGCGGTGGCGTGTGCTGACTCG
TNGGCGTCGACGCTCGTGGCAGCCACCGANCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGCGCGGTG

ACGGCCGATGAGCTGACCGAGGTGACAGCGCCGTGTTGGCTGACTTGAACCGACATGGAGTCGCCCCGGTTGGCGT
CACCTCAAGCATTTCAATGGTTATGCGACCAAGTTTTTGGGTTACGCCGTGACACATCACGTCGGAGACTTGGATGAGC
TGTGTCTGCCAGATAGCCCCGAATCGGGACGACCGTGGTCACGGTGCGTCTGACCACTCGGGTCGGGTCGCCCCGCGT
ATCGGCATGGGTGCGTNATCACAGCGACACGCGCTGCCAAGGANGTNCGGNCGGACC (SEQ ID NO. 52)

::::::::::Rv124T7D4.seq::::::::::
CGGGTTGCGGATCCACGCGTGCGGGTTGTGACGAGCTACGGCACTGAACCGCGCCACAGCTCGCCGATCCGCTTTCG
GTGGTTCTCGATCGACTCGCCGTAGCGGATGCGCAGCGCTGCTCGAATATCGGGTACAGCTAGGCCGGCCCTCCNC
TTTA (SEQ ID NO. 53)

Clone Rv126

::::::::::Rv126SP6.seq::::::::::
CTTGATTTTGATCATCATGACGATCATCACCTAATTTTGCTACCCGCACTGGTTATCGTGGGTACCGTCGTGCTTTC
CATGGGCGCCTCTTTCGGGCTTTCGTTATGGTCTGGCAGGACATTCTGGGTATCGATTTGTACTGGATGGTGTGGC
GATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAAAGGAAATGG
GGCCGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCATGGTGT
(SEQ ID NO. 54)

::::::::::Rv126T7.seq::::::::::
GGGGATCCCTAGATCGACCTGCAGGCATGCAAGCTTGGCGTGCTTCCAACCCGAATTGGCTTTCGGCGCCATCGGT
GAGGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGG
AAGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCG
GAGNACTGTCAAGGCGCGGTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGGTGGTGGTGGCGGTCCCGATCGGCC
CAGACGACATCGTGGCGAGATTGCGNCGGGTACGCCGATGAGGTGGTGTGTTTGGCGACGCCGGCGTNGTTCTTCGCCG
NCGGGCANGGTTACCGCAACTTCACCCAGACCTCCGACGACGAGGTGGTGGCGTCTCCTGGATCGTGCTC
(SEQ ID NO. 55)

Clone Rv127

::::::::::Rv127SP6.seq::::::::::
AAGGCTGCAGGTGCAAGCGGNTGGTTACGACTCCCTGTGTGATGGACCAGTTCTACTATCTGCGTCTACACGGCCC
TTGGTGCGCTGGCCACGGCAGCGGCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCCGACC
CTGCTGGCAAAGATNATCACACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGCGGGTTT
GAACTGGAACACCGCCAGCTCGGCTTCGAGTCCGGCACTTCCAGTGACCGGTTCAACCGGCTCGA (SEQ ID NO. 56)

::::::::::Rv127T7.seq::::::::::
CTTTCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTT
CATCCTGACGCCGGAACAAATTGACGCNCGGTTCCGCTGACCAATACGGTCGGTCCACGATGACCCAGTACTACAT
CATTCGCACGGAGAACCTGCCGCTGCTACAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGT
TCAACCAAATTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGGTTATTGACCTCGCCGNCCAATGT
TGGACTCCGTTCCGGTTGTTCCAGANGTCAGCCGGTCTGTCATCGCCGACGCTCTCGTCN (SEQ ID NO. 57)

Clone Rv128

::::::::::Rv128SP6.seq::::::::::
CGGTCATAGCCCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTGCGGGTGGTCCGCGACGCGCATGGGCCACCATCGCA
TTCACCAAGTCTGCGCGAATCACAGCACGTAGACGGTTCTTTCTAAGCAACACCGAAGTTTACGACCCGAATGC
TCCGGGAAACATGTACGGTAGGTGCGTATTCCGGTACC GGCTGAGCATTGAGCAGCCGGCCAGCACCGCACGAGC
CAGGCAATCAGCCGCCCGCCACCGATCGCGGTGACCACTGAGTCTCCGGAGACAATGCGGCCGGCACGCCGNCTC
CGGCGGCACCGCTACNGCGCCCGTGG (SEQ ID NO. 58)

::::::::::Rv128T7.seq::::::::::
GTGATGGCAGCCACCGCGACACACCGGCTGCGTACNTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGC
CCAGTGTTCCGGCCCTCTTTCGAGGTGAGGTGATACCGATTTGCGCATCCGCANCCGNCCTGGACGACAGAACC
GTGCCCTACGAGTGCTTGTGCGGGCGGGCCAAAGAACAGCTTGGCATCCTGGCGCGATTGGCCGGCGCGGCGTGGTC
GCCAAGGACGACGCCGTTCCGGTGTGATCGACGACGCGTGGGGTTACCGATCCGGAGCGACTATCAAGATGGGGG
AGGTCTCTGACACCATCGGCCCNACGGACATGTGATCGTCCGACGTGACGTCCACCCCG (SEQ ID NO. 59)

Clone Rv129

::::::::::Rv129SP6.seq::::::::::
GCGAAAGTCCGTTGGGTGCAATGATGTAGCGTTCTCCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGT
TCGGGTCGTACTCGATGTGCGGACCTTGGCGTTGACACCATCTTTGTATTGCGGCGAAAGTCGATCATCCGGTNG

CGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGACGCGGGC
GCACCAGCGACTTCTCCGGGGTTGACCGGGTGATCTCGGCGAAATCAGATACGCTGGCGCCGCGACGACCGAGCGCTCG
TGGGCTTGTNCTTGCGAATTGNCATGTCTAATCANGTCTTTCTCTACGCTCTCGTCGCCGGGCTAGGCCGCATTGCC
CTGCTCCTCCTCATCGCTTCGCTCTGCATCGTCCCCGGGCTAAGCCCGTGCCCCGAAA (SEQ ID NO. 60)

::::::::::Rv129T7.seq::::::::::
GATGGTTCGCGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGCCCGCGTCGCGGTATTGCGGGTTGGTGAAAA
GGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGGGAGTGACGATCTGATCGAGAGGATTGAGGGCGGGTGGCT
GGAATTCGATGCCGCGATCGCGAACACCGGATCAGAATGGCCAAAGTCGGTCGCATCGCTCGGGTCTGGGTCCGCGC
GGCCTGATGCCCAACCCGAAACCGGCACCGTCACCGCCGACTCCCCATGGCGTCCCGGATATCAAGGGCCGGCAAAT
CAACTTCCCGGTTGATCAGCAAGGCAACCTGCCTCCNCCTCCGG (SEQ ID NO. 61)

Clone Rv130

::::::::::Rv130SP6.seq::::::::::
ATACTCAAGCTTCGTATAAGACCATGGTGCGCTTTCTTTACCCCGTCCAGAGTCGGGGGCATCCGCACCGGGCTCGCA
TCGCATCATCTCCACGACGGGCCGCTCATCAGCTTGGGCCATTTCAATGTACTTGATACCCCGCGCTGCGGGTAGG
CCACTGCGACAATTCAAACACGGTGTACACGGTGAATAGTGTGAGATGGGCTCTGATCAACCGTCGCAACCCCGT
TTCGCATCAATAGCGGAATCCACCGGGTTGCATGGAGGCTGCTGACCTTGGAACAAAATTTTTTCATTACAACAA
AACACCGCCNCGGAACTTTGCA (SEQ ID NO. 62)

::::::::::Rv130T7.seq::::::::::
CGAATTCGCGGTGCACCGCTATGGGTTGCAGCAGCGGCTGGCGCCGCACACCCCACTGGCCCGGGTGTTCGCCCCG
AACCCGGATCATGGTGAGCGAAAAGGAGATTGCGCTGTCGATGCTGGGATTGCCACCGCGAGGCCATCGACCGATT
ACTCGCCACCGGGGTGCGAGAGGTGCCGAGTCCCGCTCCGTCGACGCTCCGACGATCCATCCGGCTTCGCGCGTCG
GGTGGCGGTAGCCGTCGATGAAATCGCTGCCGGCCGCTACTGCAAGGTGATTCTGTCCGTTGTGTGCAAGTGCCTT
TCGCGATCGACTTTCCGTTGACCTACCGGCTGGGGCGTCGGCACAACACCCCGGTGAGTCTGTTTTTGTGAGTTGG
GCGGAATCCGTGCTCTGGGTTACAGCCCCGAACCTGTCACGGCGGTGCGCGCCGACGGAGTTGTTATACCGATCCGT
TGCGCGTACCGCGCCTTGGG (SEQ ID NO. 63)

Clone Rv132

::::::::::Rv132SP6.seq::::::::::
TCAGACTCCACCCAGCCAGCAGCGAGCGAAGCTGAATCCTCCAACCGGGTTGTCGATCCGGACAGGTTGGGGTGCG
TTTGGGGCAATGACAGGTGGCGGCGGTGCGTTGCGGTGCGCCGGCGGAGGTGCTGCGTTGGGATCGCCCGGCTGGGCA
TTCNGCGTGTTGGCGGCGGGTGGTGGGGGGGCAACAGGTGTCGCCGGTGCGGGTGGCGCTGCAGCGGTGCACGGC
GGCGAAGCGGCCGTTGTGGGTACCGGGGGCGCTGGTCCGGATCGGCGTTGGCGGTGCGGGGCACCGCAACGGTCAAC
AAGCTGGCGCTGGCCATCGCCGCGATAGCCAGTGCCGCCAATCGTCCCTTGCAGCGTGTCAAGTNGGGGTCCACCTGA
TGCATGGCCAAAGAACCTACCGTGTTAACGGCNCACNCAAGGACCGCGCGGTGCGN (SEQ ID NO. 64)

::::::::::Rv132T7.seq::::::::::
TTTCCGCGGTACCCGCTCAACTTTGTGTCNACCCTCAACGCCATTGCCGGCACCTACTACGTNCACTCCAACCTACTTC
ATCCTGACGCGGGAACAAATTGACGCAGCGGGTCCGCTGAACAATTCCGGTCCGTCCCACGAAAGAACCAGTTTNCNT
CTTNCACGGAGAACCTGCCGCTGCTAGAGCACTGCGATCGGTGCCGATCGTGGGAACCCACTGGCGAACCTGTG
TTTCAACCAACACTTAGAGTGTAAATTGTAAACCTGGGCTAGGGGAAACCGGCTCTAGTTTTTCCACCNCTCTCCGCCCC
NTGTTTCGAATACTCCGTTCCGGTTGTCCCCAA (SEQ ID NO. 65)

Clone Rv134

::::::::::Rv134SP6.seq::::::::::
GCTTCCGGCTCGTATGTTGTGTGGAATTGTGACCGGATACCAATTTACACAGGAAACAGCTATGACCATGATTACGC
CAAGCTAGTTAGGTGACACTATACAACTCAAGCTTGCCGGTGGTGGGCCGACCACTTCGATGGCACGACCCGTGA
ACTGCTGCCCGGCAATTCTTCTGGTCCGCCGACCGATGGACCGCGGCTGGGATTCAGAAAGGTGCCCGATCCCGC
CCCTGGGAAAACCGCGTGACCTTACTTCACGACCAACGAC (SEQ ID NO. 66)

::::::::::Rv134T7.seq::::::::::
CCGATCGACTGATGCGCCGACAACCACGCCCCAACAACTGGAATGAACCGTCGTGACCATCATCAGCACGCGGTTGTA
GGCGACTTGCGACATGTTCAACCCGCGTACTCGGACGGAATCTTCAAACCGAAACAGCCAGCTCGGCCAGGCCTTT
CACGTACTCGTCCGGGATCTGGGCACCAACGCTCGAGGACGCTGCCGTCCACGGTGTCTAGGAATTCGCGAGTTTGAC
CAGAAACGCTCGGTTCCGGCCCTCCTCGGCGTCCGACGGCTGGGAAATGGGTGTATGAGCCCTACGGGAAACCGGCC
CACAAAGAGTTCTTTGGCGAAGGACGGTTATCCCAACCACTTTCGCGAGATTCTCGGCAAGGGCCCCGCGCTTGCTC
CTCGGTGACCTGAGTTTGCTGTGCCATCGCCGCTCCTCCCTGA (SEQ ID NO. 67)

Clone Rv135

:Rv135SP6.seq::

TGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTTACGGTGATCGCGCATCACCTGGTTCATGAAGTGAAGC
AGCGCAGCGCTTCTCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGTTCGGGTGCAGGTGCTCGGGCAGCTCGG
CCGCGACAGCCGCTGACCCCTGAAACAGCTTCCATATCCCGCGACGAACGACGCCAGTCCGCTACGTAACCCCTCCG
CGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCGGGTGTGGGGTGTTCGGCGACCGGCAGCCAGGTG
GTCCACACTGCCGACGGGCGCCGCGAGCCGTTACCGACAGGCCGCCGAGCAAGTCCGCCGATCGCATACTCC

(SEQ ID NO. 68)

:Rv135T7.seq::

GGGGCGCTGCTGGTATAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGCGGTACGTGCCATCGA
GACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACGAGCAATCGCGGTATGCGTTCCTTGAGCATGAGTCGGCGAC
CGTCGTCATGGTCGACACCCAGCAGCGAAAGACGCAGATGCCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGAC
CTCTGCTGACCGGCATGTTTGGTCGCGATGCCTGGCGCCCGCGCGGTGGTCTGGTTCGGCTCGGATAGCGAGGT
CAGCGAATTCTCGTGGCAGCTCGAAAGGGTCTGCCGGTGCCTGCTTTGCGCAAACGATGGCGCAGGTTACGGTCCG
CGGGGTTCGGGCTGGCGGCGCCAGAGCACGAGTTACCGATGCGCAGCTAGTGGCGACAGCGCTCAGCCAAC

(SEQ ID NO. 69)

Clone Rv136

:Rv136SP6.seq::

TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCCGTACAGGTGCGCTCCAACACGGCGGGGAAGCGACACCA
GCCTACCGAGCTTGGAGTCCAGGACGCCAGCGGCGGCGTTCGGTCTGCGTCTGGTGGCGCCGGGTGGCGTTGGCTGG
CAACGATCTCCACCCAGCCGCTCGGGTTACCCACGATCTCGGCATAGACGCGGGCCGAGGCCGGTGCATACCGTATT
GCGTCAATTGGGACGCGGTTGTGCATTTCGGCTAGCTCGGTTGCCACACCCGTCAGGGGTTGACGTTGGCGGGTTCGG
CGGGCCCCAGCACCGCTGTCAACATGCCCGCCAAGCCGACCTGCGGCGCCACCACT

(SEQ ID NO. 70)

:Rv136T7.seq::

CGGCATGACCACCGACAGGCCGACTGGTTCGTACCACTCGAACGCCGGGTGTTGATGTCCAGCCGCTGAAGTCGTC
CTGCGCGCGCAGGCCGTCGAGCAGGTACAGGGCGGGCGAGTTGGCACCACCACTTTGGAATTGGACCTTGATGTCAGC
GCCATCGACGGCGACGGCACCTGCAGGTACTCCACCGGCAAGCCCGCGGGGAAATGCCCGCGGTTCGCCGTGCC
ACCGACGGCGCCGACCAGACCCGACACTAGGGCCGCGCCGACGGCCCCGACCACGAGTCGACGCGACATACCGTGAC
GGCGCCACGAACCCTGTCAACAAGCTGCATTCTTGCTTCCCTCATCTCAACGCATCCATGCATGTTTGGGCG
CATCCTGAATTANGTCAGACTGCAGGCGCTGGGCGGCGAGTGCTCGTGTATCAACCACAACCTTCGGGCGT

(SEQ ID NO. 71)

Clone Rv137

:Rv137SP6.seq::

TTCCAACCCTAATTGGCTTTTCGGCCCCATCCGTGAGGACGGGGTGCGGGTGCTCAACAACAACGTCGTCCGCGGGACA
CACCTCTATGCTGCCGCCATGGACGCGGTCCAACGCAAGCAGCTGATCGAGCTACAACCCCGCGCGGAACGCTTCCGC
CGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGCC
AAGGCGCGGTGCCAGCTCGCCGGGCGCACGGTCGGGACAAGGTGGTGTGGCGGTCCCGATCGGCCCAAACGACATC
GTGGCGAGATTTCGCGGGTACGCCGATGAGGTGGTGTCTGGCGACGCCGCGGCTGTTCTTCGCCCTCGGGCAGGGT
TACCGCAACTTCAC

(SEQ ID NO. 72)

:Rv137T7.seq::

CAGGCATGCAAGCTTTCCGCCGATACCCGCCATGTGCGGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCG
GGATCCCAAAGTGCGGATGATCGGGCCGCCTACGTCTGGTGTACCTCGTTCGTAACAACGAAACCGAAGCGTATGAC
TCGGTCAACGCGGTGCGGCACATGGTGGACACCAACCGCACCGGCGGGAAGGCTATGTACCGGTCCGGCA
GCACTCAATGCCGACAGGCCGAGGCCGGAGACAAAAGTATCGCTAAGGTACCGCGCATCANAGCATGGTATGCG
AGCAATGTTGCTAGTGATCTATCGCTCCGTAATTACCGCGGTTCTCGTCTTGATCATGGTCGGCATCGACTCGGCCAA
TCCGCGGATTCTATCGCCTTGCTCGCGGAACACAACATTTTACCTTTACATTTGCACCAACCTGCTCTTCTCAT

(SEQ ID NO. 73)

Clone Rv138

:Rv138SP6.seq::

CACTACTCAAGCTCTCTCNTATTACCAACCCCTGTAATTTGGGATGGGCAAAAAGGCGAAGCACCGCTTGGCCACNAA
CGCCGGGAGGGACAATCTCGGGCGGCTATGGCTTCTCCGGGAAGGCCCAACGTACGGCGTTTCAACACGTGCGGTC
GCCCTCCGACCGCAACATTCGGGGATTGGCACCAACCTGNTACCAACCTGGCCGGGCGATGATCTGCAGCGTCGCCG
CGGGTAGTCCCCGCCCGGGCGGTACAGTCTGAAACCCCGATGACCATCGATGTGTGGATGCAGCATCCGACGCAACG
GTTCTTACACGGCGGATATGTTCTCTCGCTGCGCCGGTGGACCGTGGGTCTATCCCTGAAACCGACATCCCN

(SEQ ID NO. 74)

.....Rv138T7.seq:.....
CAGGCATGCAAGCTTTCGTCAAGTTCATTGCGCCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGG
CCAACGGTGATTCTTGGCCGCCGCTGACGGCGGAACGACGCCAGCGACCACATTACAGCAGATGGCCAGCGCGTGCC
GGGCCACGAGGTTGGTGCTCGGCGGCTACTCCAGGGTGCGGCCGTGATCGACATCGTCACCGCCGCACCACTGCCCG
GCCTCGGGTTCACGCAGCCGTTGCCGCCCGCAGCGGACGATCACATCGCCGCGATCGCCCTGTTTCGGGAATCCCTCGG
GCCGCGCTGGCGGGCTGATGAGCGCCCTGACCCCTCAATTTCGGGTCCAAGAACATCAACCTCTGCAACAACGGCGACC
CATTTGTTTCGGACGGCAACCGGTGGCAACGCACCTAAGCTACTTGCCCGGGATGA (SEQ ID NO. 75)

Clone Rv139

.....Rv139SP6.seq:.....
GTTTATGCACTGGTTAGGTGTTTCCATGAGTTTCATTCTGAACATCCTTTAATCATTGCTTTGCGTTTTTTTATTAAA
TCTTGCAATTTACTGCAAAGCAACAACAAAATCGCAAAGTCATCAAAAAACCGCAAAGTTGTTTAAAAATAAGAGCAAC
ACGTACAACAAGGAGATAAGAAGAGCACATACCTCAGTCACTTATTATCACTAGCGCCCGCCGACGGCTGTAACCGAG
CATAGCGAGCGAACTGGCGAGGAAGCAAAGAAGAACTGTTCTGTGATAGCTCTTACGCTCAGCGCAAGAAGAAATA
TCCACCGTGGGGAAAACTCCAGGTAGAGGTAC (SEQ ID NO. 76)

Clone Rv13

.....Rv13SP6.seq:.....
ATACTCAAGCTTGGGTGTAGCCGATCACCGGAAGTCNCATGATCAGCCACGTTCCGCGCCGCCCGGCATACGGTGGTG
TACCGATCTCCGCGTCATACACCCGCGGTAATCGCCGACGGTGCCGTTTCGCGAGCCGAA (SEQ ID NO. 77)

.....Rv13T7.seq:.....
AGCTTTATCGAAAGCGCAACAGCTCGCGCGGCCACGACGTGCTGCGTCGGATTGCCGGCGGCGAGATCAATTCCA
GGCAGCTCCCGGACAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTCAACCCGGTGCCCGGGTTCGTGGTG
ACCTGCCGATCGCACAGGTTGGCCCAACCGGCCGCTTGATGCCCGGTTCGGCAAGCCCGGCAGTTGCCAAACCCATC
GTGATCAGGCTCGGCTCGCGAGTTTCGGCGAAGAAATGGTTTCGCTGATCACCTACCATCGGCCA (SEQ ID NO. 78)

Clone Rv140

.....Rv140SP6.seq:.....
TCAACACGCCCGCAGCCACCACGCGGGTCGGGCGCCGGGCCCTCCAGGCTNCTCCGCTCGGTGATGGCACG
CCACCGCGACACCACCGGCTGCGCTACGTCGAGCCATACCGGGCGGAGCTACATCGGCCCGGCCGCCAGTGTTCCG
GCCCTCTCGCCAGGTTCGAGGTCGACACCGATTTCGCGCATCCGACGCCGACCCCTGCGACGACAGAACCGCGGCCCTA
CCCCTGCTTGTGCGGCGGGGGCCAAAGAACCAGCTTGNCATCTGCCACAATTGGCCGGCGCCCG (SEQ ID NO. 79)

.....Rv140T7.seq:.....
CAGGCATGCAAGCTTCACGTCCGTACGGCTCGGGTACGCTTCGGTCGCAGTGTCGAGTGATAGATGACGACCGGGAC
CTCGTCGGCATCTTCATAGCCCGCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTAGAAGGTCGGCCAGCGCTC
GGCATTGGTTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGACGGCTTCGTGGG
GTGGTCGCGACGCGCATGGGCCACCATCGCATTACACAGGTCTGCGGAATCACCAGCACGTAGACGGTTCCTTTCTC
AAGCAACAC (SEQ ID NO. 80)

Clone Rv141

.....Rv141SP6.seq:.....
AATATTCAAGCTTTCGGCGGAAACGGACNCCTTGCGAACATTGATAACAAAATAGAAATCATTGATGGTTTGAGTCAC
CAGGCCGATCAAGCCTTCGCCGAGCCAAATTCGAATCAAGAGGCCCAAGCCGTACCAATCAGCCCGGCAACGAGGGA
TTCCGTCNTTATCAGCCNAAATAACTGCTCTCGGGTACCACCCAAACAGCGCAATATGGCGAAAAACGGTTCGCCGTTG
CACAACATTAAATGTCTCGGTATTGTTGATTAAAAAGATACCCACCACAGGGCAATCCAATGAGAGCGGTTAAAT
GACCGTAAAAACCTCCCGTCATCTGTTT (SEQ ID NO. 81)

.....Rv141T7.seq:.....
CAGGCATGCAAGCTTGTGTCATCTTCTGTGACTGCTCCCGAAACCTGGGGGTGTGCCTGCTGTGTATGCACGGCATA
CGGACATCCTTCCCCTGATACCCGCGGTGCAACCGAGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGAC
GGCAGGCCAAGTTCGCCGACCGTTAACCTAGTGCTGTTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTTCGGCCGTTA
GGAATGAATTGAAACTCAACCGATTGTTGGTGCCGCCGTAAGTGTCCTGTCTGCGGGTGCGCTGGTGTTCGCCGCTGT
GGTAACGACGACAATGTGACCGGGGGAGGTGCAACCACTGGCCAGGCGTCCGCGAAAGTCCATTGCNGGGGGAAGAAG
ACAC (SEQ ID NO. 82)

Clone Rv142

:Rv142IS1081.seq:::

GAAAGTGCCCCAAGGTGTTGGTGAAACTCGCTGGACGGTCCCCAGGATGTTGGCAGCACATTACCCGGACATGACCGG
AGCAAGACCGGACATCCTCCCATACCGTCGTCGCCGTGTACATCCGTAGCCCCCTCTGGCAGGTGCTGGGTTGAACAA
AATCAGCCCAACACCTGCCACGACGAAGAAGCGGGTTGCGCTGGCATGTCTTGTGCGCTCGGCGATCGAATTCTACGA
ATTCTTATCTACGGGACCGCTGCGGCGCTGGTGTTCACCCGTTCTTCCACACCTGGATCCCACGGTGGCCGC
CGTGGCCTCCAAGGGACATTGCTGTGGCGTTCCTATCCCGGCCGTTGCGCGCGGCCGCTTTGGATACTTTGGAGA
CCGCTCGGCCGCCAGAAGACCCTGGTCGCCACACTGTTGATCATGGGCCTGGCAACCGTGACTGTTGGGCTGGTTCC
ACGACAGTGGCCATCGCGC (SEQ ID NO. 83)

:Rv142SP6.seq:::

ATATTCAAGCTTTGTACACCAAGTGTCCGACCAANCCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT
CGCCACCAAGCTGGTCAGTGCGCGTTCATCTCGCTTGGCGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG
CAGCTTGGGGATCGCGACGTGATGGTTGCGGCACGGGTGTGCAAAATCAGGTGGCGGTAGCCGTTGCGCTGATTGGA
CCGCTCATCGTTCGCTTCGCGGTAGCCNCCCGCACAGGGCGTCGGCTTCAGCCCCATCCAAGGCGGCGATGAACG
TCGAGAGCAGCCCGCGCAGCAAATCCGGGCTCGCTGTGCGAGTTGGTCAGCCAGAAGCTGCTCGGTGCATAAGATG
AGAAGAGGTGAGTGCCTTTCTTCG (SEQ ID NO. 84)

:Rv142T7.seq:::

CAGGCATGCAAGCTTTTGAGCGTCTCGCGGGCAGCTTCGCGGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACG
GATCTGACCGAAGTCGCTGCGGTGCAGCCACCTCATTTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTG
CCGCTTGCCGACGGCGACGCGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCGACCGTGGTC
GCGGTTGCGCCGCCAAAGCGGCGGGTGGGTGCCATCATGAATGCCTCACCGCCGCCGACTGCACGGCCAGTGCCCC
GGCGATGTACGATCGGGACATCATGCTCGCTTCATACTCCTCGACAGTCCGCGGAACAGCTCCATTCCCGGACC
GCCAACGC (SEQ ID NO. 85)

Clone Rv143

:Rv143SP6.seq:::

ATACTCAAGCTTTTGGCTGGGTGCGCTTCCAATTGACGCTGCACCGCTATGGGTTGCAGCAGCGGCTGGCNCCGCACA
CCCCACTGGCCCGGGTGTTTTGCCCCGAACCCGGATCATGGTGAGCGAAAAGGAGATTNCCTGTTCGATGCTGGGA
TTCGCCACCGCGAGGCCATCGACCGATTACTGCCACCGGGGTGCGAGAGGTGCCGCGATCCCGCTCCGTGACGTCT
CCGACGATCCATCCGGCTTCCGCCGTGGGTGGCGGTAGCCGTGATGAAATCGCTGCCGGCCGCTACCAAGGTGA
TTCTGTCCCGTTGTGTCCAAGTGCCTTTCGCGATCGACTTTCGTTGACCTACCGGCTGGGGCGTCGGCACAACACCC
CGGTGAGTCTGTTTTGTTGCAAGTGGGCGGAATCCGTGCTCTGGGTTACAGCCCCGAACCTCGTCACGGCGGTGCGCC
GCCGAC (SEQ ID NO. 86)

:Rv143T7.seq:::

CAGGCATGCAAGCTTCAACCTATTGACGCAATTGTGCGAACTGACGGCGCCCGCGCATGGCCAATCCGGAAGACCATCA
TTGGCCAGTGGCCGGGCGCTAACAGGTTCCAGCCCCCACCAGTGCCGCTCGAACATGCGGTGCAACCCATTGCGAGG
CCGGCAGGGAAGCACCAGCGGAAGCCGCAAGGGCTGCAGTTCGCGGCCCAATAGTGTGCTCCGCAACCAGATGCGCT
CGAAACCCGCGCGCAGTCAGCGACCCGACGCGAGGTGAGAGACGTGTCAGCGCGCCACATGGGGTGCCAAAT
CGGCACGGCAGGTAGGCCGCGCGCAACCCCAACCGTGGTGCATGCCACGGTCCGCGAGGAGCCACCC
(SEQ ID NO. 87)

Clone Rv144

:Rv144SP6.seq:::

ATACTCAAGCTTCCCAGGCGCAGGTGACGGCGCGGCTAGCGCCACTTGATGCCGCAACCGATCGACGGNCGTTGGTC
GGGTTGACTGGCGCGCCGCGAGCAGGGCGTCAACCGCGCCCGGACGTCGGCGGCGCTACCGGTGCGCCATTGCC
CGGGCGGGAGTCTCGAGCTGACCAGGTAGACAACTCGGCGCTGGCCGTGCAAGACAAACGTGTCGGGTGTGACGGC
CGCGGAGAAGGCGCNGGCGACGTCTCGGTTTCGTGCTAGAGATACGGGAACGTCCAGCCGTGGCGCGCGGCGCTCGGC
GACCATCTGATCGGGCCGTCCTGCGGGTAGGTGACCACTCTTACTGGAGATACCGACCATCGGGACCCCTTGATC
GGCGAGGTCCCGGCCGACCGTGGCCAATCCGGCGCGCAGGTGTGCGCCGTACCGGCCAGTGGTTC (SEQ ID NO. 88)

:Rv144T7.seq:::

CAGGCATGCAAGCTTTANCANCAATCAACCCGCGCCCGCACCAGCACCAGACGATGTGATGCCATCGAGGTGAATGT
CGAACTGGCNCAACCATCTGGCGACCGCGACCCGCAACATGGGTACCGGCGATTTCCGGTGCCAATGCCGACCC
GACGGGCGGCTCTCACCAGGAGTACCTCGATCACCAGACAGCCGGCCGTTATACTACGCACCCCTACCGTGTCA
CGCCCAAACGGCGTGGTGGTGCATTGCCGAGTGACCCCGCACCAGTGTGTCGCCGATCCGCCGACCAATCC
CGCACCCAGTCGCCAAACCCGAAATACCGTGTGCGGTGGTAACTGACACCGACAGTAACGTCACTACGGCCGCC
ACGCCGACGCCGAACCAACACGCACATGATGATCGGCTG (SEQ ID NO. 89)

Clone Rv145

.....Rv145SP6.seq.....
ATATTCAACCTTGACACATTGACGATACCTTGGTCACGAGACCCCAAAGCTGGCCTCCACCGCGCGCCGGGGACCA
CGGTCATACCTTGANNNGCTTTTCGATCGTTGATGCTGCGTCTTGGTCCGCGGAAACCGCAGGCTGGCATATGCACGT
GGGCGCACTGGCGATCTGCGATCCCCACCGATTGCGCCGAATACAGCTTTCAGCGGCTCCCCAAGTTGATCATCGACC
GGCTGCCGGATATCCCGCACTTGCGGTGGCGGGTCACCGGCGCCCCGCTCGGACTGGACCGGCGGTGGTTCGTGAGG
ACCACGAAC (SEQ ID NO. 90)

.....Rv145T7.seq.....
CAGGCATGCAAGCTTCATGCCCCGCGCATGATAGCCACATGCACGCAATCGAACTCAGCGAAACCGGCGGGCCAGGCG
TCTTACGCCACCTCACCAGCGCGCAACCTCAACCCGGCCACGGAGACCTCCTGATC (SEQ ID NO. 91)

Clone Rv146

.....Rv146SP6.seq.....
ATACTCAAGCTTGATTTTGATCATCATGATGATCATCACCCGAATTGTGGTAGCCGAGTGGTTATCGTGGGTACCGT
CGTGCTTTCCATGGGCGCCTCTTTCCGGCTTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGAT
GGTGTGGCGATGTCGGTGATCCTGCTCNTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAGA
GGAAATTGGGCGCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCAT
GGTGTTCGCCGTTACCATGTCGTTGTTGTGTCAGCGATTTCGAATTATTGGTCAGATCGGTACCACCATCGGCCT
GGGCTTGCTGTTTCGACACCCTCGTCGTGCTCGTTTCATGAAACCGTCCATTGCTGCCCTGCTGGGACCTGGTTCTGCT
GGCGGCTACGGGTGCGCCCGCGCCCGGCGAGTCAAATCTTCGCCG (SEQ ID NO. 92)

.....Rv146T7.seq.....
CAGGCATGCAAGCTTGGCGTGCCGTTCCAACCCGAATTGGCTTTCCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC
AACGACGACGTCGTCCGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTA
CAACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGAC
GGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTGCCAGGTGCGCCGGCGCACGGTGCGGACAACGTGGTGCTGGCG
GTCCCCATCGGCCAGACGACATCGTGGCGAGA (SEQ ID NO. 93)

Clone Rv147

.....Rv147SP6.seq.....
ATACTCAAGCTTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA
ACATGAGCCAGCCTCTCGTCGGCGGTGCGGTGCAAGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAAC
CAGCTTCCATATCCCGCGACGAACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTT
CTCCACCGACCGGGCCCGGGTGTGGGTGTTTCGGCGACCGGCAGCCANGTGGTCCACACTGCCGAAG (SEQ ID NO. 94)

.....Rv147T7.seq.....
TAGTCGCTGACCGGTGCAGGTTTCGACNATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGCGCAGGCT
ATCGCACCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCCTGAGCATGAGTCGGCGACCGTCGTATGGTCGAC
ACCCACGACGGAAGACGAGATCGCCGCTTANCNTGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCTGACCGGC
ATGTTTGGTCGCGATGCCTGGCGCCCGCGGCGGTGGTTCGTGGTTCGGTTCGG (SEQ ID NO. 95)

Clone Rv148

.....Rv148SP6.seq.....
ATACTCAAGCTTTCCGCCGATACCCGCCATGTCGCGCACATCCAGAACTTCTGGGGGGATCCGCTGACAGCGGCGGGA
TCCCAAAGTGCGGATGATCGGGCCGCTACGTCGTGGTGACCTCGTCGCTAACAACGAAACCGAAGCGTATGACTCG
GTCCACGCGGTGCGGCACATGGTGGACACCACACCGCCACCGCACGGGTGAAGGCCTATGTACCGGTCGGCGAGCA
CTCAATGCCGACCAGGCCGAGGCCGGAGACAAAAGTATCGCTAAGGTCACCGCGATCACGAGCATGGTGATCGCAGCA
ATGTTGCTAGTGATCTATCGCCCCGTAATTACCGCGGTTCTCGTCTTGATCATGGTCGGCATCGACCTCGGCGCAATC
CGCGGATTCTNTCGCCTTGCTCGCCGACCACAAATTTTCAGCCTTTCAACATTTGCGACAACCTGCTCGTTCTCATGG
CGATTGCNGCGAAC (SEQ ID NO. 96)

.....Rv148T7.seq.....
CAGGCATGCAAGCTTGGCGTGCCGTTCCAACCCGAATTGGCTTTCCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC
AACGACGACGTCGTCCGCTGGACACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTA
CAACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGAC
GGCATCGCCACCGGAGCGACGGCCAAGGCGGCGTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGTGGTGCTGGCG
GTCCCGATCGGCCAGACGACATCGTGGCGAGATTGCGCGGGTACGCCGATGAAGTGGTGTGTTTGGCGACCCGGCG
TTGTT (SEQ ID NO. 97)

Clone Rv149

.....Rv149SP6.seq:.....
ATACTCAAGCTTTGGCATTGTGCACATTTTCCACCCGTGCTCTATTAATGCTGAGCCGCTAATTGTGACCCAGTCGG
GAAACACGCGGAGCACCAAATTCACCGCAGCGGCCGGGGCGGTTCAACTCACCATGGATCGCTCTCGTCTGTTGCTG
TGGACAATCGTCTGCTAGCGCTCGCGAACACCTCAGCTTCTGCTGCCGCGGCTTCTTCCGGCGATGGTAACCCCA
GGTTTCGCCCACGGTCTTACGTAGCAGTGCGACGCGGTGTTTCATCTGCATCGACCTGTTGACTCATCTGTCAAGGAT
GAAGGCGTACTGGGCGGACTGCGCCTTCTGCCGCGCCAGGTCGGCAATCACCAGGATCTCAGAAACGAGCTGCGACTC
ACTCTTCCAGGCCACCTGGCCGAAAGCTCGACATGGTCAATCCGGCCG (SEQ ID NO. 98)

.....Rv149T7.seq:.....
CAGGCATGCAAGCTTGGCGGCCGAGTGGTTTCGACGGCCGCTCGCTTCTCGGCATCGGTTTGGGCTGTACCAGCAG
TTGGTAGTTCTTTCACGTACTGTTGTTTCGAGCGTCGAGCCGCCGCGCTGTGAGGTCGCCGACGCGTATCCCGCCAG
GCCGGTCAGGGTGCCCTTCCAGTCCACGCCGCTGTGGTCGGCGAACCGCTTATCTTCAATCGAGACGATCGCCAGCTT
CATCGTTTGGCGATCTTGTCCGAGGGCACCTCGAACCGGCGCTGCGAGTACAGCCACGCGATCGTGTGTCCTTCCG
GTCGACCATCGTCGATACCGCAGGCACTTGCCCTC (SEQ ID NO. 99)

Clone Rv14

.....Rv14SP6.seq:.....
ATACTCAAGCTTCCCGCGGCCAGTACCGAAAGCGCGAACAGCTCGCGGCAGCCACGACGTGCTGCGTCGGATTGCC
GGCGGCGAAATCAATTCAGGCAGCTCCCGGACAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTCACCCCG
GTGCCCGGGTCTGTTGTCACCTGCCGATCGCACAGGTTGCCCCACAACCGGCCGCTTATGATCCCGGTCGGCAAGCCC
GGCAGTTGCCAAACCCAGCGTGATCAGGCTCGGCTCGCGAGTTTCGGCGAAGAAGTGGCTCGCCTGATCACCTACCATC
GGCCAGGATCTGCGTGTATCACAACGCTCGCCAAGGAGGTTGTTGTTGGTGTATCGACGGCCTTTAGCCAGATGTTT
GGAATCGACTATCCGATAGTGTCCGCGCAATGGACTTGATCGCCG (SEQ ID NO. 100)

.....Rv14T7.seq:.....
AGCTTCGGTGTAGCCGATACCGGAAGCCGCATGATCAGCCAGTTCGCGCGCCGCCCGGCATACGGCGGGCTACCGAT
CTCCGCGTCATACACCCGCGGTAATCGCCGACGTTGCCGTTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAG
TTCCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGCTCAACGACGTCAATCACGTTGTCGCTTTCTACGGTCACCGA
CCCGGTGACCGTAGTGCCTCGGCTCGGCGGAGAAGTTGCACCGCCACCACCGCGACACCGTCTTGACGCGGGAC
GCCACCCCGGATCGGTTGTTGGCCAAGGTAATTGGGTCAATTCATTTGACGGGACGCCGACCCCGCAGCCCCAGTAC
CGCCACGACCACGCGGCTGACCCACCACTGTACGAACCAAGGCGACGCCG (SEQ ID NO. 101)

Clone Rv15

.....Rv150SP6.seq:.....
ATACTCAAGCTTCGGTGGCTTCGCCCCGCTGCGGGTGGACTTCATGACAACGCGGGGGCGATTACCCCGCTACCG
CCAGCAGCATGACGGCGGTACCTAACACCGCCCGGATGCCTCGACGTGCCTCGATGTGCTCACGGAATCGCCCCGGC
ACCGCGATCTCGAGGATCACCAGGTTACCCCGGCGAGCGGACACCGACAATTCGTACACCGCCACGCGGATCCGG
CCCTGGGCCAGCTGATTGGAGCTGGCG (SEQ ID NO. 102)

.....Rv150T7.seq:.....
CAGGCATGCAAGCTTCCACATGTACGGATCCACGAACATCCCGTTGAACTGACAGGTGCGGCCCGGCTCGATCAGGCC
GGCCACTTGTCTACGCGGTTACCGAAGATCTCTTCGGTGACCTGCCCGCCGCGGCCAGCTCGGCCAGTGCCCGGC
GTTGGCCGCGCGGCGGACGATCTTGGCGTCCACGGTGGTCCGGGTCTTGCCCGCTAGCACGATCCGCGAGTCGGCCGG
TCACCCGGGT (SEQ ID NO. 103)

Clone Rv151

.....Rv151SP6.seq:.....
ATACTCAAGCTTTCCAAGTCCCAAGTGTGATCATGGCCAAAGAGCTCGACAAAGCCGTAGAGGCGTTTCGGACCCGC
CCGCTCGATGCCGGCCCGTATACCTTCTCGCCGCCGACGCCCTGGTGCTCAAGGTGCGCGAGGCAGGCCGCGTCTGTC
GGGTCGACACCTTGATCGCCACCGCGCTCAACGCCGAGGGCTACCGAAAGATCCTGGGCATCCAGGTCACCTCCGCC
GAAGACGGGGCCGGCTGGCTGGCGTTCTTCCGCGACCTGGTCGCCCCGCGGCTGTCCGGGGTCGCGCTGGTACCAGC
GACGCCACGCGCGGCTGGTGGCCGCGATCGGGGCCACCTGCCCGCAGCGGCTGGCAGCGCT (SEQ ID NO. 104)

.....Rv151T7.seq:.....
CAGGCATGCAAGCTTACACGTAGCGCGCTCGATAAATGACTCCGCGCGCTTCGCACATCCTCGTAGCGATCCTTG
GCGAGCAGGTCAACCGGGCGCTGCCGTCGAGGAGCCGGTTTTTGGCGTGACGCACTGGCCGACACCTCGGGGGGTA
AGCGAATCCGAGAGCAGGAGGACGAGGTACGAAGCTGCGCCAGCCGCTCGTACCGCTCAGGGCGGATGTGCGCGGTC
CGCCACCCCGGTACCGCCGATCGGACACCTGTATGACCGCGGCGACGTC (SEQ ID NO. 105)

Clone Rv152

:::Rv152SP6.seq:::

CGCGGGCGGCATTACCCCGCTACCGTCAGCAGCTTGACGGCGGTAGCGAACACCGCCGGATGCAGCGCAGGTGCGT
CTATGTGCACACGGAATCGCCCCGGCACCGCGATCTCGAGGATCACCAGTGCCCGCCCCCTG (SEQ ID NO. 106)

:::Rv152T7.seq:::

GGGATCGAGGAACAGCGCGTTGAAGTATAGGTGCGGCCGCTCGAGCAGGCCGGCCATTGTTCGATGCGGTTACC
GAAGATCTCTTCGGTGACCTGCCCGCGCCGGCCAGCTCGGCCAGTGCCCGCGTTGGCCGCCGCGGCGACGATCTT
GGCGTCCACGGTGGTGGGGTCATGCCCGCGAGCAGGATCGGCGAGCGCGCGGTGAGCCGGGTGAACCTTCGTCGAGAG
CTTGACCTGCCGTGGGGAGGCGAACCACGGTGGTGGTATCTCGACCAGGCCCGGGCAACCTCGGGGGTGGCGCC
GACGGTGAACAGGTTGCGCTGGCCACCGCGGGTAGCCGCCGGCACTATGCCGATGCCAGGCCGCGGATCACCGGTGC
GGTCAGTCGGGTGAGGATGTGCCCCGGCCCCAGGTGCAAGATCCAGCGGGCGCCGGCGCGTGGACACNGGTGATCTC
GTCCACCATCGACTTTCTGATCA (SEQ ID NO. 107)

Clone Rv153

:::Rv153SP6.seq:::

TAACTCAAGGCTTGCGTTGAGGCCCCAGGCCCATCGACGGTTTGGCGGCCTTAAATGCACTGAGGTGCTCAATTGACC
CCACAGCGGAAATGCCGACTATTTCGAGGCCCTCCTTCGCTTGGCTGCCGGAGAGGGGCTCCGCGGGAACCGCATGCA
GGTATATGACCTCGGTTTCTCGGTGCTACCGGTGCTTGTTCGAGGATGAACCTCGGCGTTGGAATTGTCCAGCCGGC
CCAAATTCATCGAGCGCAGATTTCGTACACATGGCCGGCGCGACATACGCTTCACCGTGGATCTGCTCCACACGGACCG
CCCTGTCCGGATCCTGCTCACGGGTAAAGGAACCTTACNTGGCNCTCGGTGCC (SEQ ID NO. 108)

:::Rv153T7.seq:::

CCTTCTGCGCCACCCACACCGTCAACGCCCCGCAAGTCGACGTGCTCCAGGCCATCGGCGGCCTCACGGATGGATTCCG
GCGCGGACGTGGTGATCGACGCCGTGCGCCGACCGGAAACCTACCAGCAGGCCCTTCTACGCCCGCGATCTCGCCGGAA
CCGTTGTGCTGGTGGGTGTGCCGACGCCGACATGCGCCTGGACATGCCGCTGGTTCGACTTCTTCTCACGGCGGTG
CGCTGAAGTCGTGCTGGTACGGCGATTGCCTGCCCGAAAGCGACTTCCCCACGCTGATCGACCTTGACCTGCATGGCC
GGCTGCCGCTGCAGCGGTTGTTTCCGAACGCATCGGGCTCGAAGACGTCGAGGAGGCGTTCCACAAGATGCATGGCG
GCAAGGTATTGCGTTCCGTGGTGATGTTGTGATGGCCGCCATCGAGCGGTCATCACCACGG (SEQ ID NO. 109)

Clone Rv154

:::Rv154SP6.seq:::

ATACTCAAGCTTGATTTTGATCATGATGATCATCACCAGAGTGTGGTAGCCGAGTGTTATCGTGGGTACCGT
CGTGCTTTCCATGGGCGCCTCTTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGAT
GGTGTGGCGATGTGCGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTCCCGGTTGAAAA
AGAAATTGGGCGCGGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGTTACCGCTGCCGGCAT
GGTGTTCGCCGTTACCA (SEQ ID NO. 110)

:::Rv154T7.seq:::

ATTGNCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGACACACCTCGATGC
TGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGA
CCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGCAAGGCGGCGTG
CCAGGTCGCCGGGCGCACGGTGCGGACAAGGTGGTGTGGCGGTCCCGATCGGCCAGACGACATCGTGGCGAGATT
CGCCGGGTACCGGATGAGGTGGTGTGTTGGCGACGCCGGCGTTGTTCTTCGCCGTGCGGCAGGGTTACCGCAACTT
CACCCAGACCTCCGACGAAGAAGTGGTGGCGTTTCTGGATCGTGCTC (SEQ ID NO. 111)

Clone Rv155

:::Rv155SP6.seq:::

ATACTCAAGCTTTTCCCGTCCGTCATCGCCCAAGCGCGTGAGGCCGAAGCGGCTGGTTACGACTCCCTGTTTGTGATG
GACCACTTCTACCAACTGCCCATGTTGGGGACGCCCCGACCGAGCGATGCTGGAGGCCTACACGGCCCTTGGTGCGCTG
GCCACGGCGACCGAGCGGCTGCAACTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCTGCTGGCAAAG
ATCATCACCACGCTCGACGTGGTTAGCGCCGGTTCGAGCGATCCTCGGCATTGGAGCGGTTGGTTTGGCTGGAACAC
CGCCAGCTCGGCTTCGAGTTCGGCACTTTCAGTGACCGGTTCAACCGGCTCGAANAGGCGCTACAGATCCTCGAGCCA
ATGGTCAAGGTTGAGCGCCAACGTTTTTCGGCGATTGGTACCCACCGA (SEQ ID NO. 112)

:::Rv155T7.seq:::

CGGCCACCGGGGCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTC
CGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTCATCC
TGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTC

GCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAAC
CAAACCTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGGTTATTCGACCTCGCCGCCCAATGTTGCGA
CTCCGTTCCGGTGTGTTCCAGAGGTACGCCGGTCTGTCATCGCCGACGCTCTCGTCGCCGGGACCAGCAGGAATCGG
CGATTCGCTACA (SEQ ID NO. 113)

Clone Rv156

:Rv156SP6.seq:::

ATACTCAAGCTTGGGGTGGCGCTGTCGGTGGTGTGCTTGGCGGCGTGGTATCAACACCGCCACGAAATGGGGCAC
AAGAAGGATTGCTGGAGCGGTGGCTGTCCAAATCACCTCGCCAGACCTGCTACGGGCATTCTACATCGAGCAC
AACCGTGGCCATCACNTCCGGGTGTCCACACCGGAGGACCCGGCGTGGCGCGGTTGGCGAAACGTTGTGGGAGTTC
CTGCCCCGAGTGTATCGGCGGCTTGGCTCGGCCGTTTATTGGAGGCCAACGGCTGCGTGGGCTCGGCTCAGC
CCCTGGAATCCCATGACGTATCTGCGCAACGACGTGCNCAACNCGTGGCTGATGTGNGTGGTGTGTTGGGGTGGG

(SEQ ID NO. 114)

:Rv156T7.seq:::

TGCGCACCGCACCGCGGCGAACGCTCAAAGGCACCTACTGGCACCAAGGCCCCACACGTCACCTGTGACCTCCTGCG
CCGACCCCGCCGAGGTCTGGCCGTTACCACCGAACGGGCGAGCCGGGAGTCTGGTACGCATCGAACAAAGAGCAAG
GTGCATGGGCGGAGTTGTTCCGCCACTTCGTGATGACGGGTCGATCCATTGAGGTCCGTGCGCGCGTGGTTCGAG
TGGCGGTACACTCCAGGTACTCGACCTCACAGACGAGAGGACTCGATCCCATCTAGGTGTGGACGAAACAGATCTTC
TGTCCGACGACTACACCACCCAGGCCATCGCCGCGCCCGCGATGCCAACTTCGACGCGGCTACTGGCCCCGGCGG
CGGCGCTCCCGGTTGTCAAACACTTTCGGCTGTTGTTACGCACTGCCAACATCGAGCCCGA (SEQ ID NO. 115)

Clone Rv157

:Rv157SP6.seq:::

ATGAAATAAGAAGAGCACATCCCTCAGTCGGTTATCATCACTAGCGCTCGCCGCACCCGTGTAACCGATCATAGCGAG
CGAAGTGGCGAGGAAGCAAAGAATATCTGTTCTGTGATAGCTCTTACGCTCAGCGCAAGAAGAAATATCCCCCGCG
GGAACAACCTCCAGGTAGAGGTACACACGCGGATAGCCAATTGAGTAATAAACTGTGACACTCACACCTCATCAAT
GATGACGAACACACCCGATATCCGTCACATGACGAAGGAAAGAGAAGGATATCATCTGTGACAACTGCCCTCA
AATTTGGCTTCCTAA (SEQ ID NO. 116)

Clone Rv159

:Rv159SP6.seq:::

ATACTCAAGCTTGTGCAACTCCTTCTTGAATACCGGCCGCCATCCACAGATGCCCGGAAGAACTTCCAGGTACCCAT
GGCGGCTGGATCAGGGGGCGGCACAGTTGGTCTTGTCTCGAGTGGCGTGGTGTCCGGCTTGGACGGGGCTCC
GACGGTACCGGAGGGCAGCGACAAACACTTATGCACTTGGGCGACCCGCCGAGACGGTGGCAGACCCATCCCGACGG
CACAAGCTCAGCCGCGGCCGCTCTTGTCTTCTGTCGGATCGACATTACCCACTTCTGACCGGGCTTGGGCGAAGGAA
GCAGAA (SEQ ID NO. 117)

:Rv159T7.seq:::

GGTATAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGCGCA
GGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTATGGT
CGACACCCACGACGGAAAGACGACAGATCGCCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCTGAC
CGGCATGTTTGGTTCGCGATGCCTGGCGCCCGGCCGGCTGGTCTGGTTCGGCTCGGATAGCGAGGTACGGAATTCTC
GTGGCAGCTCGAAAGGTCCTGCCGGTGGCGGTCTTTGCGCAAACGATGGCGCAGGTTACGGTTCGCGCGGGGTGCGGC
CCTGGCGGCGGCCA (SEQ ID NO. 118)

Clone Rv15

:Rv15SP6D2.seq:::

GACACTATATNATACTCAAGCTTCAGGTCAATGTGCGCCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCGCCGGAN
CCCTNTCTAGA (SEQ ID NO. 119)

:Rv15T7.seq:::

CTGTAGCCACCTGTTGCCATCCCCGTCATGCCCGACTCTGGTCATCTCGGATCCGCTGACACCCCGCTAAGGCTGCTC
CTCTCGGTGCATTACCTACCGACGGCGAACNCCCCAGCTTTACGACTATCCGGATGACGGCACCTGGTTGCCGGCT
AACTTCACCGTCAGCTTGGACGGCGGCGTACCGTCGATGGCGCCAGCGGGGCGATGGCCGGGCCCGCGACCGATT
GTCNTCANCCTGTCGCGTGAACCTGCCGACGTCATCGTGGTGGTGTGGGCACCGTGGCATTGAGGGCTACTCCGGC
GTCCGGATGGGTGTCGTCAAGCGCCCGACCGGCAGGCCGA (SEQ ID NO. 120)

Clone Rv160

:Rv160SP6.seq:::

ATACTCAAGCTTCGCACGCTCGGCGCGCGCGGTACCGCCAGGTCGCCAACAGATCGTCGATGTTTCGCGTCGTCCGC
CTCGCGCACGTGGTCTGTCAACAGTCAACGTTAACGCCGCCGCACATGTCCTGCGGCGGGGCAAAACGTGAAAAACG
AGCGGGCGACTGCNATGTCATGACACCGACGGCCGCGATGGGCCCAGGGTCTGGCAAATTCGATCTGTGCGGCCAGT
GCCAGCAGCTCGCCTCGTCATACGGCCGGCCGACGAGTTGAACCGCATGGACGTGAGAGCAGCCCGCGCAGCAGA
GGCACCACGGGCGCGGGTGGCCGGTCAGATTCAAAATTGAAAGTACGGAACCGCTGCACCACCA (SEQ ID NO. 121)

:Rv160T7.seq:::

ATCGTTTCGACCAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGTCGCCACCACGCTGGTCAGTGCG
CGTTCAGCTCGCTTGGCGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCGCAGCTTGGGGATCGCGACGTCG
ATGTTGCGGCACGGGTGTCAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGACCGCTCATCGCTGCGTTTCGCGG
TAGCCCGCCCGCACAGGGCGTCGGCTTCAGCCCCCATCAAGGCGGCGATGAACGTGAGAGCAGCCCGCGCAGCAGA
TCCGGGCTCGCCTGTGCGAGTTGGTCAGCCAGAAGCTGCTCGGTGTCGATAAGATGANAAGAAGTCATTGCGTTATTT
CCT (SEQ ID NO. 122)

Clone Rv161

:Rv161SP6.seq:::

ATACTCAAGCTTGGGTGTTGCGATCACCGGAAGCCGATGATCAGCCACGTTTCGCGCGCGCCGGCATAACGGCGGCG
TACCGATCTCCGCGTCATACACCCGCGGGAATCGCCGACGGTGCCGGTTCGCGAGCCGAAGGTGACGACGCTGATTG
AATCGAGTTCAGGTCCAGCGGTGGCGCAGCAACGGCGCGAGCTCAACNACGTCAATCACGTTGTGCTTTCTACGG
TCACCGACCCGGTGACCGTAGTCGCCCCGGTGCCTCGGCCGAGAAGTTGCACCGCCACCACCGCGACAACGTCCTTGCA
CGCGACGCCACCCCCCGGAT (SEQ ID NO. 123)

:Rv161T7.seq:::

GCGCNAACAGCTCGCGGCAGCCACGACGTGCTGCGTCGGATTGCCGGCGCGCAGATCAATTCAGGCAGCTCCCGGA
CAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTCAACCCGGTGCCCGGGTCTGTTGTCACCTGCCGATCGC
ACAGGTTGGCCCAACCGGCCGCTTGATGCCCGGTGGCAAGCCCGGAGTTGCCAAACCCAGCGTGATCAGGCTCG
GCTCGCGAGTTCGGCGAAAAAGTGGCTCGCCTGATCACCTACCATCGGCCAGGATCTGCGTGTGATCAGGACGCTCGC
CAAGGAGGTTGTTGTGGTGCTATCGACGGCCTTTAGCCAGATGTTCCGAATCGACTATCCGATAGTGTCCGCGCCAAT
GGACTTGATCGCCGGCGGTGAGCTGGCTGCCGNGT (SEQ ID NO. 124)

Clone Rv162

:Rv162SP6.seq:::

ATACTCAAGCTTTCTCCGATACCCGCCATGTGCGGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGGAT
CCCAAAGTGC GGATGATCGGGCCGCTACGTGCTGGTGTACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTCGG
TCCACGCGGTGCGGCACATGGTGGACACCACACCGCCACCGCACGGGGTGAAGGCCTATGTACCCGGTCCGGCAGCAC
TCAATGCCGACCAGGCCGAGGCCGGAACAAAAGTATCGCTAAGGTACCCGCGATCACGAACATGGTGATCGCAGCAA
TGTTGCTAGTGATCTATCGCTCCG (SEQ ID NO. 125)

:Rv162T7.seq:::

CCATGAGCACCGCCAGCCGAGCAGAGGCCAACTCCGCCGACGAGGCCGGTTGGACTTGTGCTGCTGGACAAGGGG
TTTAGCCGCGGAAGCAGTGACGTACATCGGCGAAGAGCAGTTGCGCTGTCGACCGACGGCGCAAACCGTGAGGCTAGG
GAAGCGAGGAGCATGGCCGCCGACCCGCAATGTACACGCTGCAAGCAAACCATCGAACCCGGATGGCTATACATCA
CCGCCATCGCCGCGGTCAAGCCGGGATCGTCGATGACGGCGCAGTACTGATTACGTGCCCGGTGAATGCCGCACCC
CGGGGAGCACTTCCGCCAAAATAACCCGGTTGG (SEQ ID NO. 126)

Clone Rv163

:Rv163SP6.seq:::

CGGGTGTGATTGGCCACCGGCGGCGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTTGCTGAGGAGTGCTGAACCG
TAGTCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGGAGCGCGCAANTGAATCCTCCAACCGGGTGTGTCNATC
CGGACAGGTTGGGGTGCCTTTGGGGCAATNACAGGTGGCGGCGGTGCGTTTCGGGTGCGCCGGCGGAGGTGCTGCNTTG
GGATCCCCGGTGGGCATTGCGGNTGTTGGCGGCGGCGGTGGTGGGGGGGGCAACACGTGTCNCCGGTGCGGGTGGC
CCT (SEQ ID NO. 127)

:Rv163T7.seq:::

CCAAGATCTACCATCGAATACGACGGCTGCGGACTTTCCGCGGTACCCGCTCAACTTTGTGTCGACCCTCAACG
CCATTGCCGGCACCTACTACGTGCACTCCAATACTTATCCTGACGCCGGAACAANTTGACGCAGCGGTTCCGCTGA

CCAATACGGTCGGTCCACGATGACCCAGTACTACATCATTCGCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGAT
CGGTGCCGATCGTGGGGANACCCACTGGCGAACCTGGGTTCAACCAAATTGAAGGTGATTGTTAACCTGGGCTACGG
CGACCCGGCCTATGGTTATTTCGACCTCGCCGCCCAAATGTTG (SEQ ID NO. 128)

Clone Rv164

:Rv164SP6.seq:::

AGTTCCCGAGTTTCGGCTTTGGATCAAGACCCAGTCCGCGGGCGCGATCCGGCNGCTCGGTGACTACATCAAGCCAC
AAATCGACGGCTTTCGGGGTGCCGATACCGATGACGTGGCGGATGTCGAGTGTGAGTTCTCGGCGGGGCGGATGCTC
ACCTGGCGATCACCTGCCTCTCGTTGACGATCGATCGTCTATGCCGCCGTCTCTCGGGGAACAGGCCNCCAGTACATC
GCCACAGACGGGATCCACCCGATTTCGGCTACGGTTGCTCGTTTCGGTGTTCGGACTAGTCGGTCTGTTGACGTGC
CGGTGATGCGGACCGGTCTAGCACTGACCAATGGCCAAAATGCGGGC (SEQ ID NO. 129)

:Rv164T7.seq:::

CGGGGGCCTCTTAATAGTGTAGGAAAGAAGCTCTACATATTCAGGAGGATTCACCATGGCTCGTGCGGTCCGGATCG
ACCTCGGGACCACTCCGTCTCGGTCTGGAAGGTGGCGACCCGGTCTGTCGTCGCAACTCCGAGGGCTCCA
GGACCACCCCGTCAATTGTGCGGTTCCGCCCAACGGTGAGGTGCTGGTCTGCCAGCCCGCAAGAACCAGGCAGTGA
CCAACGTCGATCGCACCGTGCCTCGGTCAAGCGACACATGGGCAGCGACTGGTCCATAGAGATTGACGGCAAGAAAT
ACACCGCGCCGAGATCAGCGCCCGCATTCTGATGAAGCTGAAGCGCGACGCCGAGGCCTACCTCGGTGAGGACATTA
CCGACGCGGTTATCACGACGCGCCGCTACTTCAATGACGCCCGAGCGTCAGGCCACCAAGGACCCGCCAGATCGCCGG
TCTCACGTGCTGCGG (SEQ ID NO. 130)

Clone Rv165

:Rv165SP6.seq:::

ATACTCAAGCTTCATAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGGC
CGCACCGCCGGCATCTCCCGGTACGCGAGGCGCGGGCCCGCCGCGCAGCGACGGCGTGTTCGCGCAGTTCCGCCGTCA
ATGATGCTGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCTTCGCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCG
ACAGCCACCACCCGAGTGGCGACCAGTGTCCACCACGGACCGCAGCGATGCCGTACCTCACCCGTCCAGCGGTCC
ACCACGACACGGTCTGTCACCAGCGCGGGGCAATTCACCACCCAGGCGGTACCCGCCAGGCCGATCGCCACACCCGCC
ACCATCCCCGATGCAGCCAGGCCGGGAGTAAGA (SEQ ID NO. 131)

:Rv165T7.seq:::

CTGGTGCTGGACGGAGCCTAGTACAACCTCTCTCCAATGCTCTTGCCCCGATCGCGGCGACCAGGATGACCCAGGAC
ATCCTGCCGCCCGAAGTACTGGAAAAGCTCACACCCGAGTTCTGTCGCACCGGTGGTGCCCTACCTGTGCACCGAGGAG
TGTGCCGACAACCCATCGGTGTACGTCAGTGGTGGTTAGGTGCAGCGAGTTGCGCTGTTTGGCAACGACGGCGCC
AACTTCGACAAACCGCCGTCNGTACAAGATGTTGCGGCGCGGTGGGCCGAGATCNCCGATCTGTCCGGTGCGAAAAT
GCTGGATTCAAGTTGTAGAACTAAAT (SEQ ID NO. 132)

Clone Rv166

:Rv166SP6.seq:::

ATACTCAAGCTTTCCGGCGTCTCCACCTGACCCAAAAAGCGCAGGTGCGCCGCCAAACGGCCCGCTGGCCGCGCA
ACTGGTCGGCGTCGCCGTGGCCGACAATCAGTAGCTGGACATCCGGAACCGCTGCACCACCTTCGGCAGCGCGTCAA
GCAAAAACGGCCATTCC (SEQ ID NO. 133)

:Rv166T7.seq:::

TTTCAGATCTATTTTTATGACATGACTGGAGATCTGTCTAGATTGCAGCTCCTGTGAGCGTGGGTACCGGATTCAAG
CCGGTCGGTCACGCCGCGGTGGTACCGGCTTTCGCGGAGTGTCTGGCCTCGAGTTCGGCGATCGCGCGGAAGTGCCT
TTCGCGCACCAAGATCGCGGCCTAATGGCCGGCGATGACCGCGATGACCAGCGGATCCAGGAAAAACCGTTCCAACC
AGTGCTGGGCGGCCATCCCCG (SEQ ID NO. 134)

Clone Rv167

:Rv167SP6.seq:::

ATACTCAAGCTTCCCGACCACAAGTTGAACAGCACCGATTTCCGGCGAGCACTTCGTCAACTTCAGGGTGCCCGCACC
AAGTATTTGCAACAAGTATTTCCGTCCGGGCCCGCCGCCCGCGCGGCGAGGTGGTCATCTGGCGGCGGGGCTGGAC
TCCCGCGCGTACCGGCTGCCTTGCCCGACGGGACACGGTTTTTGAAGCTGGACCGCCCGCAGGTCTTGATTTCAG
CGCGAGGTGCTCGCCAGCCACGGTGGCCAAACCGCGCGCCCTGCGCCCGCA (SEQ ID NO. 135)

:Rv167T7.seq:::

GTGTGCTGTCAATTCAAGAGCTGAGCCTGATGCACTCAACTTACTGAGCATGCTAACGCTGGTCTGCGGGTCTTGTTT
CCGCGTGTGCGCAGGGCACACGCTCGGGCGTAGCTGGGAGAGGCCCGGTCAAGCCCGAGAGCAGTGCTCAGTCCG

CCAGCTTGACCGACTTTTCGATGAGAACGCGCTTCTCGCCGTATTGAACTGGCGTGCTGACGGTCGCTGAGCAGCGCTC
GCCGAGTGCGGCCGTGATTCTTTCATCGAGCCAGGAGGCGCATTCGTGTTTCGGCCGCTGCGGGTCGGCCCCATCGT
CGACGCGATCCGTACCCCACTCCTCGATCAGGTCTGCCTCATCGAACGGGCCAACGGTGCTGTGCGGAGTATGTGTGCG
TGGGCACGGCGAGCCGGGTGCTGTGGTACACCCACCGTTGCATGACCAAGTTGACGCCTGACTGGCTGAGCACC GCGA
TCCGCTCACAGGTCGGAACGTTGGTG (SEQ ID NO. 136)

Clone Rv169

.....Rv169SP6.seq:.....
ATACTCAAGCTTTTGGTCTAGCCGGCCGAGCCCGATACAGGTGTCATTGGCCACCGGCGGGCGGTGTCCGGGAAATGG
CGGGTCCCCGGTGGTTTTGCTGAGGAGTGCTGAACCGTATGCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGCAGG
CAGCGCGAACTGAATCCTCCAACCGGGTGTGATCCGGACAGGTTGGGGTGCGTTTGGGGCAATGACAGGTGGCGG
CGGTGCGTCCGGGTGCGGCCGGCGGAAGTGCTGCGTTGGGATCGCCCGGTGGGCATTCTGCGTGTGGCGGCGGCCGG
TGGTGGGGGGCAACAGGTGTCTCCGCTGCGGGTGGCGTGCAAC (SEQ ID NO. 137)

.....Rv169T7.seq:.....
GGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGACTTTCCGCGGTAC
CCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACCTACTTCATCCTGACGCCG
GAACAAATTGACGACGCGGTTCCGCTGACCAATACGGTCCGTCACGATGACCCAGTACTACATCATTCGCACGGAG
AACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACTTG
AAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGTTATTTCGACCTCGCCGCCCAATGTTGCGACTCCGTT
GGGTTGTTCCAGAGGTGAGCCCGGTGTCATCGCCGACGCTCTCGTCGCCGGGACCCAGCACGGAAT
(SEQ ID NO. 138)

Clone Rv16

.....Rv16SP6.seq:.....
TTCTNTCTTCCNNATTCTGNNNTCTCNTACTACCNNGGCCNCAAAACACCTTGGCNAACGCTCAAAGGCGNTACNGG
CACCAAGGCCCCACACGTACCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCTTGGCCGTTACCACTGAACGGGC
GAGCCGGGAGTCTGGTACGCATCGAACAAAGAGCAAGGTGCATGGGCGGAGTTGTTCCGCCNCTTTTTTATGACGGG
GTCGATCCATTCGAGGTCCGTGCGCCGCTCGGTGAGTGCGGGTCACACTCCAGGTACTCGACCTCNCAGACGAGAGG
ACTCGATCCCATCTANGTGTGGACNAAACAGATCTTCTGTCCGACGACTACACACCACCCAGGCCATCGCCGCCGCC
GCGATGCCAACTTCNACNCCGTNCTGGCCCCGGCGCGGCGCTCCCCGTTGTCAAACACCTGCCGTGTTGTTTACN
CACTGCCCAACATCNAGCCCGANCNATCCNAGGTCCGTCCAACGCCTCCGCGGCTCNCCAACCTNCTCCNCTGATCN
TCCGACCAAAACATGCCGACTCCNTGCNCCNATTGCTTGNATCCCT (SEQ ID NO. 139)

.....Rv16T7.seq:.....
CCGTATCGGTGCGTGTGCTTGGCGGCGTCGGTATCAACACCGCCACGAAATGGGGCACAAGAAGGATTGCTGGAG
CGGTGGCTGTCCAAGATCACCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCACAACCGTGCCCATCACGTC
CGGGTGTCCACACCGGAGGACCCGGCGTCGGCGCGGTTTCGGCGAGACGTTGTGGGAGTTCTGCCCGCAGTGTTATC
GGCGGCTTGCCTCGGCCGTTCAATTTGAGGGCCCAACGGCTGCGTCGGCTCGGCGTCAGCCCCGGAATCCCATGACG
TATCTGCGCAACGACGTGCTCAACGCGTGGCTGATGTCGGTGGTGTGTTGGGGTGGGCTGATCGCGGTCTTCGGCCCC
GCGCTGATCCCGTTCGTATCATCCAGGCAGTCTTCGGCTTCAG (SEQ ID NO. 140)

Clone Rv170

.....Rv170SP6.seq:.....
ATACTCATGCTTGCCGAAGTTCCGATGGGTGCGCCGGCGGANCCCAGCGAAGTCGCTAGCGTGCCCGTGTCTTGGCT
TCGGATCTATCCTCGTACATGACCGGCACCGTGTGGACGTGACTGGCGGCGCGTTTCATATGACACCGAGATCATTCG
CACGGTACGGCAATTTCGTCAAGAAGGAAATCTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA
AATCGTCGATCGGCTGGGTGTTATTGGCTTGTGCGGTGCGCGGTCGAAGGGTATCGACACCACCGAGTTATTCTCC
GGCGTGCC (SEQ ID NO. 141)

.....Rv170T7.seq:.....
GGCGTCAACGGTGTGCGCACCGGCGTCTGCACTTGGTAGGCCTGCACTTGTGCATCAGGCCGATGCCGCGGCCCTC
GTGGCCACGCTGTACAGCACACCGCGCGCCCTCAGCGGCGACCATCGCCAGCGCGGCTCCAGCTGAGGCCCGCA
ATCGCAGCGCGCTGACCCAAACACATCGCCGTCAGCACTCCGAATGCACCCGGACAGCAGTCGTCACCGTCGGC
GTTGGGCCCGCGATCTCGCCGCGGACAGCGCGACATGTTCCACGTCCTCGTAGATGCTGGTGTAGCCGATGGCGCG
AATCTCCCATGACGAGTCGGAATCCGCGCCTCGGCG (SEQ ID NO. 142)

Clone Rv171

.....Rv171SP6.seq:.....
ATACTCAAGCTTCGGCCTCGCTGCAGGAGTGGGAGCCGAGGGCTGGAAATCCGAAAAACGAGCCGGTGATCGCACTG
TCGCCGATCGGGGCCGACCTGGTTGGTGTACCGATGAATCCGCACCCAAAATGTGGCTGCGGTGGCGTTTCTTGAC
TCCTTGGCGTCTGACTCTTGTGGCAGCCACCGAGCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGGCCG
GTGACGGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGTTGGCTGACTTGGAACCGACATGGATTGCCCCGGTTGG
CGTCACCTCAAGCATTTCAATGGTTAT (SEQ ID NO. 143)

.....Rv171T7.seq:.....
ATGCGTCACCCGATGCGCCAGATCGGGGCTTCGCAAATAAAGCACGAACAGGCGGGCAAACGTCTATCTCGGAGC
CGGAAGGGCAATCAGCCGACCGTCGACGAACGACACCGGCGATAACCACTTAGGCGTTGAACGGCCGGCCCAAACATT
ACGCCTCCGTTGATAAGGCTTTGGTCTCTTCCCCGGTCATCCAAGCACCTTGGCGCAAATTTGAACGCTTCTCTGT
CCGGGACCGGCCCGGGGCTTTGGGGTCCNTCCGA (SEQ ID NO. 144)

Clone Rv172

.....Rv172SP6.seq:.....
ATACTCAAGCTTCAATCGCGCCGCCACAATCCAAATATGCGTCTAGCGTCTCGATGAGCGTCGGTCCGGCATCGGCTA
GGGGCCGCATCAGTCGGTATGACAGGGCCACGATCGCCCAAGGCGTCGCCCATCAAGGGCGCGTTCGGGCAAAAATTC
CCCTATCCAGCACGGGCCGCGGCGCTCCGCNCCAGCCGGCGACGGCGTTCATCCCGGAGATCGCCTCGCTAGCGCTGC
GGTGCGCCGCGGTGAGCATGGGCGCCGTGGGGCCGATGACCACCGGGGCGT (SEQ ID NO. 145)

.....Rv172T7.seq:.....
TTCGGCGGGTCTGTAGATTGCGGTGCGCCACCCACAGGCACTCATGAACCGCAGCCACGATCGATCTCGGTGG
(SEQ ID NO. 146)

Clone Rv173

.....Rv173SP6.seq:.....
GCGCACCATCGCCAGTAGGTGCCCGTGGTTCGGGCGCTCGAGCCACCCGAGCGGAAACGCGAGTCCGAACAGCAACAG
CAGGACGGGCGCAACCAGGGCGGTGACCATGCCCCGCGCTGAACATCAACCACAGGAAGGGCTCCGCCGAGCGTCC
GCGCGACC (SEQ ID NO. 147)

.....Rv173T7.seq:.....
CATCGTCGAACTTCGGTCCGGGTTGNTAGNACCGCAGCACCAAACGCACCCACCGACCCCCACGCTTCACGCCAACCC
TTAGTTCAATTGGCGTGAACAGCAGCGTAGCCGGTTGCCCGATATATGTGGAAAAATCGTTCGGACGTACAAAAAAA
GTTCTTGACGCTGGCGTCAACTCGAAACTGCCTCGGAAGTCAATGATGATCCATCAGTCAATATTAAAGTCG
(SEQ ID NO. 148)

Clone Rv174

.....Rv174SP6.seq:.....
ATACTCAAGCTTGTCTGCTGCCTCAGCGTATGCATCCAACAGCGCATCGCGATCAACGATCAGGCGCGCGGATTTCGG
GCCGCGGGCAGTGGCACTGGCCAGATGGCCGTTTTTTTCGAGAACTTCAACGCCTGAGCGCTGCTTCCCATCGAGAG
ACCGGTGGCCTCTACAAACCGATGCGACAGTTGGACCGCGATGTTCCGACGAGCGCTTACATACGGCAAGTNTGGC
GCGG (SEQ ID NO. 149)

.....Rv174T7.seq:.....
TTGTCCAGGCGGGGAATCGGGCAGGGAGACGACCTTCGTTTCGGTTCGATCGTCGGAACGGGTAGTTGGCCGCGAC
CACGTTGTTTCGGGTCAGCGCGTTGAAAAGTGTGCACTTGCCGACGTTGGGCAGGCCACGATCCCCAGGCTCAAGCT
CACAGA (SEQ ID NO. 150)

Clone Rv175

.....Rv175SP6.seq:.....
ATACTCATGCTTGGCGCCTGGGTGGCAGCCACCTGCCACACACGACCGCGGTGCGGACGCGGCTGACGCGCCTG
GTGGTCAGCATCGTGGCCGGTCTGCTGTTGTATGCCAACTTCCCGCCGCGCAACTGCTGGTGGGCGGGCGGTGGTTGCG
CTCGCATTGCTGGCCTGGGTGCTGACCCNCCGCNCAACACCGGTGGGTGGGCTGGGCTACGGCCTGCTATTTCGGC
CTGGTGTCTACGCTCTCGTTGTTGCCGTGGATCGGCGAGCTGGTGGGCCCCGGGCCCTGGTTGGCACTGGCGACGACG
TNCGCGCTGTTCCCCGGCATCTTCGGTCTGTTCCGCGTCTGGTACCTGTTGCCGGGTTGGCCC (SEQ ID NO. 151)

.....Rv175T7.seq:.....
CGCCAATTCAGGATATCGTTAACCGATATCCCGAGCCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGGCGCTGCGAC
GAAAGGTGTGACCGTCATGAAACAGACACCACCGGCGGCCGTGGCCGCTCGTCACCTGCTCGAGATCTCAGCATCCGC

AGCCGGTGTGATCGCGCTTTCGGCGTGTAGTGGGTGCGCGCCGACCCCGCAAAGGCCGGCCGACACAACCCCGGA
ACAGGAAGTCCCGGTACCGCGCCCGAAGNACTTGATGCGCGAACNCGGAGTGCTCCAAACGCATCCTGCTGAT

(SEQ ID NO. 152)

Clone Rv176

.....Rv176SP6.seq.....

ATACTCAAGCTTGGGCACTGACTTCGGTACCCCTCCGCTTTGGCCAGCAGCAGCCACAGCGCGGTTTCGGGACCGA
ACGTGGACATCAATAGCCCGGAATCGGTGTGTGCAAGTTGGTAAACGGTGTGATCCCAAGCTTTGCCAGCCTTTTCG
TAGTCTTGGGCCCCACACCCACAGTGCTTCGACGGTACGGTACCCATGATGGCCATCCAGTTGGCATCGGTGAGCT
GATAAATGCCAGCTGGTTTCGCCAACCCGGTAGCGATCTTGGCGCGCTGCTTGTGTCACTGATACCTATCGAGCAAG
ACAGCCCGGTTTGGCAGAAAATGACTTTTCGGATCTCTTCGGCGACTTCGATGGGGTTCGTCGGGA

(SEQ ID NO. 153)

.....Rv176T7.seq.....

AAAGTCCTGTGCCGGTTCGCTAAACACCCGGCGGACACTCAGACGGTGTGGTGGTGGCGCATGGCACCAGCGGGCAGC
AAAGCGCACTTCTCCGGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGGTCTGCGCAGGCAGAAACGTTGGTACA
CAGCTGCTGGCGTTTCGGCGCCACCGATGTTTATGCCGCGGACCGGGTTCGCTGCCACCAGACGATGGAGCCACTCGCC
GCGGAAGTGAACGTGACCATAACA

(SEQ ID NO. 154)

Clone Rv177

.....Rv177SP6.seq.....

ATACTCAAGCTTGGGTTCCACGCCCCGCGCAGCCACGCCGTACCTTTCCACGAGACCTCACCTGCCGATCCGAAATGG
AATCGGCCGTGACGGAATTGGCGCACCGAACACCCAACGAGGTGGTGGCTTCGTCGCGAACCGTCACCCGATCGCGG
CCACCGTGCGCACGGCGACGTTCTACACCCGACCAAGATCCGAAAGCTGCAAGCTCCAGCACCGATCCCGACGTCA
TCACCGCTGCCGCCCCGGCACGTCCTTGACCTATTGAGCTGGATCGGCCCGTCCGGTTGCTGGGAGTGGGTTAGAAC
TGGCCTAGAACCGCGGGGCACACCGCNCCTGGGCGGGGCGAATTCTTGACCGCNCGGCC

(SEQ ID NO. 155)

.....Rv177T7.seq.....

CGCGGTTGGCGTAGTTGGACGGGTGCGCCTCCGAGGCCAATGATGACGATGACCACGCCGATCACGATGGCCACCGAG
AGGGACAACACAGAAAGCTGACGAATCCCTCCTTGGCGGCCGGGGCTTTGTGGTTCGCCGGTTCGCGATGGGCGCGAAT
TTACGGCCCCGCTCCCCAGGCCCGCGGAAGCAGGGTCCCCAGCCAGTTGGCGTAGGCGGAATTAACGATCAGCGCCA
CCGCGATAACCTGCCATGCCTCGGGCATATCGATGTGCGGCCAGAACAGGCCGAAC

(SEQ ID NO. 156)

Clone Rv178

.....Rv178SP6.seq.....

CCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACG
ACGCCAGCGACCACATTCAGCAGATGGCCAGCGCGTGCCGGGCCACGAGGTGGTGTCTCGCGGCTACTCCAGGGTG
CGGCCGTGATCGACATCGTCACCGCCGCACCACTGCCCGGCCTCGGGTTACGCGAGCCGTTGCCGCCCGCAGCGGACG
ATCAGATCCCGCGATCGCCCTGTTGGGAATCCCTCGGGCCGCGCTGGCGGGCTGATGAGCGCCCTGACCCCTCAAT
TCGGGTCCAAGACCATCANCCTCTGCAACAACGGCGACCCGATTTGTTGACGCGCAACCGGTGGCGAGCGCACCTAG
GCTACGTGCCCGGGATGACCAACCAGGCGGCGCGTTTCGTGCGGAGCAGGATCTAACCGCGAGCCGCCCATAGATTCC
CG

(SEQ ID NO. 157)

.....Rv178T7.seq.....

TAANACCGTGTAATTTGGGATGGGCAAAAAGGCCAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGC
GGCTAGGGCTTCTCGCGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGGTGTCNCCTCCGACCGCGAACATTCCG
GGATGGCAGCAACCTGGTAGCNCCTGGCCGGGCGATGATCTGACGCTGCGCGCGGGTAGTCCGCCGCCCGGGCGGCT
ACAGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCTTACACGGCGATATGTTCCGC
TCGCTGCGCGGTTGGACCGGTGGGTCTATCCCGGAGACCGACNTCCCGATCGAAGCGACCGTCTCTCGATGGACGCC
GGCGCGTACCCCTGGGTTTGTACCGCCTGGCGTGGCCCCAA

(SEQ ID NO. 158)

Clone Rv179

.....Rv179SP6.seq.....

GTCCGCAAAAGACTCAGCGGCCGACTTTGCTCGCAGCTGGCGGTACCGCGCCACCGATTGATGCCGTGGTTCGCGGAA
GAATGCTTCCCGAAATCGCACGGCCGACTCCAGTTTCGGCGAGCATCCGCGATGCCAGCTGCGGCTGCGCCCTGCCGGC
CACGGCACCCACATGCGGCAGTTTCGTCCACCTGGGCCAGCGCCCCGCCCGGAAGTCCAAACAATAGAACTGCACCCG
GCCCGCATCGTGGGTAGCAGCCAACGCCATGATCAGCGTCCGCGAGCGCGTTGACTTGGCGTTTGGCGTGCACCTAC
GACCGCGACATTGCCTGCGGCCCCGGACAAGTCGATCGTCAGCGGCACCCN

(SEQ ID NO. 159)

.....Rv179T7.seq:.....
CTGGCCACGAACGCCGGGAGGGACANTCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCA
ACACGTCGCGTCGCCCTCCGACCGCGAACATTTCGGGGATGGCAGCAACCTGGCAGCTACCTGGCCGGGCGATGATCTG
CAGCGTCGCCCGGGGTAGTCGCCCGCCGGGCGGCTACAGTCTGAAACGCGATGACCATCGATGTGTGGATGCATCATC
CGACGCAACGGTTCTACACGGCGATATGTTNCCTCGCTGCGCCGGTGGACCGGTGGGTCTATCCC (SEQ ID NO. 160)

Clone Rv17

.....Rv17SP6.seq:.....
ATACTCAAGCTTTGCGGCGGGCGCCGAAATGTGAACGCACCAACCCGCCCGCTGCGGGTGGCGGGGCCACTCGACCT
CGAATTTGCGCGCGGTGACCATCCAGCCCGACGGCAGTTGGGACCCCGCCCCCGGTGCGGGCATAACTGTTGGCGT
CGCCGTCATAAAGCTCGAACAGCACCAGAACCGACTCCACCACCGGCCGGTGCAGCTCAAAATCCACGCCGATCTCCA
CATACCGGGAAACGTCGGTGTCCCATCGGGTTTCGGCTTGCCCGCCAGCTGCACACCACCGGTGGCCTCGGCCACCT
TCGCGGCCTGAGCGCAGCTACNCATCTGACGATCATCACCCCGCCCCCGGCTCACGCTTGCCCTCCGTGACCGCACG
CATCGCCCGGTTGCGCGCACCGCGACGCCGTACAGCCGCGCGCAC (SEQ ID NO. 161)

.....Rv17T7.seq:.....
AGCTTGCCGGGACTGCGGAACAGAAGCGGCGGTTCTACCGCGGTGTGCGGCCGGCGCGATATCGGCCTTTTACTAA
CCGAACCCGATGTGGGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATGACGGCCAGGCTTACGAGC
TTGAGGGTGTGAAGTTGTGGACCACCAACGGTGTGGTAGCGGACCTGCTAGTGTTATGGCGCGGGTACCGCGCAGTG
AAGGGCACCGAGGGGAATCAGCGCCTTTGTCGTGAGGCTGATTGCGCCGGGATCACCGTGGAGCGGCGCAACAAGT
TCATGGGACTGCGTGGCATCNAACGGCGTGACCCGGCTTCATCGCGTCNGGGTGCCCAAGACAACTTGATCGGCA
(SEQ ID NO. 162)

Clone Rv180

.....Rv180SP6.seq:.....
CTCAAGCTTGCGGATGCGGGCTGGCCAAACTGGCCGGGCGGGGTTGGCTTGTTCATCAAGGGTGGGTTGCCG
(SEQ ID NO. 163)
.....Rv180T7.seq:.....
CCGAAGGCCCGTTCCCGGGCGTTAGCAAGCGATCGTCGGTTGGCCCACTGCGGGTGAATCTTGCGGCCGCGCCGGT
CGTGGAACGCCAGGTACCCGGCGGCGTACC (SEQ ID NO. 164)

Clone Rv181

.....Rv181SP6.seq:.....
ATACTCAAGCTTTTTTCTGCTCATGAAGTTAGATGCCTGCTGCTTAAGTAATTCCTCTTTATCTGTAAGGCTTTTT
GAAGTGACACCTGACCGGGCAAATAGTTACCGGGGTGAGAAAAAGAGCAACAACTGATTTAGGCAATTTGGCGG
TGTTGATACAGCGGGTAATAATCTTACGTGAAATATTTCCGCATCAGCCAGCGCAGAAATATTTCCAGCAAAATTCAT
TCTGCAATCGGCTTGATAACGCTGACCACGTTTATAAGCACTTGTGGGCGATAATCGTTACCCAATCTGGATAATG
CAGCCATCTGCTCATCATCCAGCTCGCCAACAGAACAGATAATCACTTTGCGTAAGTGACAGAGCTTTACGACGGC
GACTCCCATCGGCAATTTCTATGACACCAGATACTCTTCAGCCGAACGCCGGTGTCTGTTGACCA (SEQ ID NO. 165)

Clone Rv182

.....Rv182SP6.seq:.....
CTCAAGCTTGGTGCCGACATGGCCGGGCTGGAGCCCGCGTATGGCAAGGTTCCGCTCAATGTGGTTGTGATGCAGCAG
GACTACGTTGCGCTCAATCAGCTCAAACGTACCCCGGTGGCGTGCTGCGCAGCATGAAGGTCGGCGCCCGCACGATG
TGGGCGAAGGCAACAGGTAAAAACCTGGTCGGCATGGTTCGAGCCCTCATTGGGCGGTTGCGGATCGGGTTGCACCGC
GCCGGAGTGCCGGTGAACCTCAACACCGCCTTCACCGATCTTTGCTCAAAAATGGCGTCGTGTCGGGGGTATAC
(SEQ ID NO. 166)

.....Rv182T7.seq:.....
CCGAAGCGTGGGAAATCCTGACCGAATACCGCGACGTGCTGGACACTTTGGCCGGCGAGCTGCTGGAAAAGGAGACCC
TGACCGGACCCGAGCTGGAAAGCATCTTCGCTGACGTCTAAAAGCGGCCGCGGCTCACCATGTTGACGACTTCGGTG
GCCGATCCCGTCGGACAAACGCCCATCAAGACACCGGGGGAGATCGCGATCGAAACGCGGCGAAACTTGGGCC
(SEQ ID NO. 167)

.....Rv183SP6.seq:.....
CGACTCGACAAGCATTCTTGACAGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACCAGATCATCTT
GGTCCGGTAGCGCTCGTCCGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCGAAAAACGCCACCGGTC
CAGCGCGTGGGCGCCCGCGGTCCCATCACAACTGAACCCCCAACAGGGGACATGCTTAGCGGTAGGGCGCGCGCCA
AGGCGGCAGCAATCGCATCACTGCGCTGCGCGTCACTATTAACCCACCCGACTTCACTTCCACGACCCCGAATGGCG
CCCGGTCAATTGATCATCTTGCGCACCGCGGATAATCCGGGATTGCCAGCCCATTCGACTACCGCATGCGAGTCATCGG
CTGACCGCAGCGGTCCGATTACCCGAGCGCCCCGANTACATCTCTCCAATATCAATGGGCGCAA (SEQ ID NO. 168)

Clone Rv183

.....:Rv183T7.seq:.....
GCGGTNTAGCTTCCCGTCGTACCGGCGACCGCCAGCCGAGAAGCTCGTTTTCCAGTGTGCTGGGGATTCTCAGCT
GCTGCTGAGTGCGTGCCAGACCGCTTCCGCTTCGGGTTACAACGAGCCGCGGGGCTACGATCGTGCGACGCTGAAGTT
GGTGTCTCTCATGGACTTGGGGATGTGCCTGAACCGGTTACCTACGACTCCAAGCTGGCGCCGTCTCGTCCGCAAGT
CGTTGCTTGGGATAGCCGGGAGGCCGGATCCGCAATGACGGATTCCATGCCAACGCTCCGAGTTGCATGCGGATCGA
CTACGAATTGATCACCCAGAACCATCGGGCGTATTACTGCCTGAAGTACCTGGTGCGGGTCCGATACTGCTATCCGGC
GGTGACGACCCCGGCAAGCCGCATCCGTGCTGT (SEQ ID NO. 169)

Clone Rv184

.....:Rv184SP6.seq:.....
CTCAAGCTTGGGCGTGACGGCCACCGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGA
CGGCGTCGCGGACTTTCCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCA
CTCCAATACTTTCATCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGAC
CCAGTACTACATCATTGCGACGGAGAACCTGCCGCTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACT
GGCGAACCTGGTTCAACCAAATTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTATGGTTATTCC
.....:Rv184T7.seq:.....
CGGGTGTCAATTGGCCACCGGCGCGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGTTTTGCTGAGGAGTGCTGAACCG
TAGTCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGCGCAGCGCAAGCTGAATCCTCCAACCGGGTGTGCGATC
CGGACAGGTTGGGGTGCCTTTGGGGCAATGACAGGTGGCGGCGGTGCGTTCGGGTCCGGCCGGCGAGGTGCTGCGTTG
GGATCGCCCGGCTGGGCATTGCGCGTGTGGCGGCGGCGGTGGTGGGGGGCAACANGTGTGCGCGGTGCGGGTGGC
GCTGCA (SEQ ID NO. 170)

Clone Rv185

.....:Rv185SP6.seq:.....
NCTTGATATTGGCGTCAACGGTGTGCGCACCGGCTCCTGCAGTTGGTAGGCCTGCAGTTTGTGCATCAGGCCGATGC
CGCGGCCCTCGTGGCCACGATGTACAGCACCGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCGTCCAGCT
GAGGCCCGCAATCGCAGCGGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACAGCACGTGCT
CACCGTCGGCGTTGGGCCCGGCGATCTCGCCGCGGACAGCGCGACATGTCCACGTCCTCGTAGATGCTGGTGTAGC
CGATGGCGCGAAACTCCCATGACGAGTCGGAATCCGCGCCTCGGCGACCCGCTCAATGTGCTTCTCGTGCTTGCGCC
GCCATTGATCAAGTCAGCAATGGTGATCAGCGCCAGACCGTGCTCNTCGGCG (SEQ ID NO. 172)
.....:Rv185T7.seq:.....
CATAAGGGCCGGCGTACCGGTACCGGCCGCGGCGCTACCACGTGCCGGAAGTGAAGCGCAGTAAGCCCTCAACGCG
CCACCGCTTTGGCCCGCGCGCCCGGCGTAGGCGCATCGGCGGTGGCCGTGGGGCGGCGCACTGCGACCTCACCAGCGG
CTTCGAGCTTTGTTTCGATCAACCGGCCAGCATGGTCGAGGATGCATTGAGACCATATTGAAATTGGTTTCATCGG
GGGCCCCGATCCGATGCCCCCTCCAGTTGCGTGAGCAAGCAGCGGAGTCGTGCGGGGATCGATGGCCACGGGGTGT
CAATGGCGGATGGTCCGCTGCCCGCCGACTGGCTCTTGCGGGAGAGCCGATCTAGCACCCAGGATCCGCGCACGTGGA
CCGAAACCGCCGAGTAGATGTCGAAAGCGT (SEQ ID NO. 173)

Clone Rv186

.....:Rv186SP6.seq:.....
CGTCCTTTTCCCAAGATAGAAAGGCAGGAGAGTGTCTTCTGCATGAATATGAAGATCTGGTACCCATCCGTGATACA
TTGAGGCTGTTCCCTGGGGGTGTTACCTTCCACNAGCAAAACACGTAGCCCTTCAGAGCCNNATCCTGAGCAANAT
GAACAGAACTGAGGTTTTGTAAACGCCACCTTTATGGGCAGCAACCCCGATCACCGGTGGAATACGTCTTCAGCAC
GTCGCAATCGCGTACCAAACACATCACGCATATGATTAATTTGTTCAATTGTATAACCAACACGTTGCTCAACCCGTC
CTCGAATTTCCATATCCGGGTGCG (SEQ ID NO. 174)

Clone Rv187

.....:Rv187SP6.seq:.....
CTCAAGCTTCATGTCCGTACGGCTCGGGTACGCTTCCGTCGAGTGTGCGAGTGATAAATGACGACCGGGACCTCGTC
GGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTAGAAAGTCGGCGAGCGCTCGGCATT
GGTCATCGGGATATGCCGCTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGAGGCTTCGTGCGGGTGGTC
CGGACACGCATGGGCCACCATCGCATTAC (SEQ ID NO. 175)

.....:Rv187T7.seq:.....
NCGCCGCCAGCCACCACGCGCGGGTCGGGCGCGGGCCCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACC
GCGACACCACCCGGCTGCGCTACGTCGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCCAGTGTTCGGGGCCCT
CTTTCGAGGTCGAGGTCGATACCGATTTGCGCATCCGCGAGCCGCACCCTGGACGACAGAACCGTGCCCTACGANTGCT
TGTCGGGCGGGGCCAAAGAACAGCTTGGCATCCTGGCGCGATTGGCCGGCGCGCGCTGGTCTCCAAGAACGACGCC
TTCCGGTGCTGAT (SEQ ID NO. 176)

Clone Rv188

.....:Rv188SP6.seq:.....
CGCCACGTTTCATGGGCAACAACCCCGATCACCGGTGGAAATACGTCTTCAGCACGTGCGAATCGCGTACCAAACACAT
CAGCATATGATTAATTTCGTCCAATTGTATAACCAACACGTTGCTCAACCCGTCCTCGAATTTCCATATCCGGGTGCG
GTAGTCGCCCTGCTTCTCGGCATCTGTATAGCCTGAGAAGAAACCCCACTAAATCCGCTGCTTCNCCTATTCTCC
AGCGCCGGG (SEQ ID NO. 177)

Clone Rv189

.....:Rv18SP6.seq:.....
ATACTCAAGCTTCAACCGATTGACGCATTGTGCGAACTGACGGCGCCCGCGCATGGCCAATCCGGAAGACCATCATTG
GCCAGTGGCCGGCGCTAACAGGTTCCAGCCCCCACCAGTGCCGCTCGAACATGCGGTGCAACCCATTTCGAGGCCG
GCAGGGAAGACCCGCGGAAGCCGCAAGGGCTGCAGTTCGCGGCCCAATAGTGTCTCGCAACCCAGATCGGCTCGA
AAACCGCGCCGGCAGTCAGCGCACCCGACGCGAGGTCGAGAGACGTCGTCAGCGCGCCACATGGGGTGCCAATCGGC
ACGGCAGGTAGGCCGCGCGCAACCCGAACGCGTGGTGCATGCCACGGTCCGCGAGGAGGCGCAGCACCCGCCAATGCC
GAAGCCACGAAACATCGGGCGCATCCACGCTTCAACCTC (SEQ ID NO. 178)

Clone Rv18

.....:Rv18T7.seq:.....
AGCTTTTGGCAGGCTCTCCTTCGAATTCGCGGTGCACCGCTATGGGTTGCAGCAGCGGCTGGCGCCGCACACCCCACT
GGCCCGGTTGTTTCGCCCCGAACCCGGATCATGGTGAGCGAAAAGGAGATTGCGCTGTTTCGATGCTGGGATTGCGCA
CCGCGAGGCCATCGACCGATTACTCGCCACCGGGGTGCGAGAGGTGCCGAGTCCCGCTCCGTCGACGTCTCCGACGA
TCCATCCGGCTTCGCGCGTCGGGTGGCGGTAGCCGTCGATGAAATCGCTGCCGGCCGCTACCACAAGTGATTCTGTC
CCGTTGTGTCGAAGTGCCTTTCGCGATCGACTTTCGTTGACCTACCGGCTGGGGCGTCGGCACAACACCCCGGTGAG
GTCGTTTTTGTTCAGTTGGGCGGAATCCGTGCTCTGGGTTACAGCCGAATCGTCAC (SEQ ID NO. 179)

Clone Rv190

.....:Rv190SP6.seq:.....
ATACTCAAGCTTTGTACACCAACTGTTTCCACCAGGCGCTCCATCCGGCGAGTGGATACTCCAGCAGGTAGCAGGT
CGCCACCACGCTGGTCAGTGCGCGTTTCAGTCTCGTTGCGGCGCTGCAGCAGCCAGTCCGGGAAATAGTGGCCTGGCG
CAGCTTGGGGATCGGCACTTCTATGGTTGCGGCACGGGTGTGAAATCACGGTGGCGGTAGCCGTTGCGCTGATTGGA
CCGCTCATCGTTCGCTTCGCGGTAGCCCGCCCCGCACAGGGCGTCGGCTTCAGCCCCCATCAAGGCGGCGATGAACGT
CGAGAGCAGCCCGCGCAGCAGATCCGGGCTCGCCTGTGCGAGTTGGTCAGCCAGAACCTGCTCGGTGT (SEQ ID NO. 180)

.....:Rv190T7.seq:.....
CCTTAAGCCCCGAGGGCCCGGCACGCGCGGTACCGCCAGGTGCCCCAACAGATCGTCGATGTTGCGCTCGTCCGCC
TCGCGCACGTGGTCTGTACCAAGTCAACGTTAACGCCCGCCGCACATGTCCTGCGGCGGGGCAAAACGTGAAAAACGA
GCGGGCGACTGCAATGTCATGACACCGACGGCCCGCGATGGGCCAGGGTCTGGCAGATTGATCTGTGCGGCCAGTG
CCAGCAGCGTCGCTCGTCATACGGCCGGCCGACGAGTTGAACCGACATGGGCAGGCCGTGCGCGTCGAAGTCCCACG
GCACCACGGCCGCGGGCTGGCCGGTCAGATTCCAGACTTGAAAGTACGGAACCCGCTGCACCACAGCAGCAACGTG
AAACTGCACCCCGCGGTTGGTAGGCGCCGATGCGGGACGGGCCGTCGCGCGCCTGGCGTCACAACTACGTCGACAT
CGTCGAAGATCGACTGGATCGGCTGCTCACACCACTCGGCGGCCGAGGCCGCCATCCGCCGTC (SEQ ID NO. 181)

Clone Rv191

.....:Rv191SP6.seq:.....
AGCTTTTTGAGCGTCGCGCGGGGACGCTTCGCGGCAATTCTACTAGCGAGAAGTCTGGCCGATACGGATCTGACCG
AAGTCGCTGCGGTGCAGCCACCCCTCATTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTGCCGCTTGCCG
ACGGCGACGCGGTGGGTGGTCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCGACGCTGGTCGCGGTTGCGC
CGCGAAAGCGGCGGGTCGGGTGCCATCAGGAATGCCTACCGCCGCGGCACTGCACGGCCAGTGCCGCGGCGATGTCA
GCCATCGGGACATCATGCTCGCGTTCATACTCCTCGACCAGTCGGCGGAACAGCTCGATTCCCGGACCGCCAGCGCA

TTGGTGATGGAATCGGCGAACTTGGCCACCCGCTGGGTGTTGACATCCTCGACGGTGGGCAATTGCCCCGGTAACGT
TTGCCGCCT (SEQ ID NO. 182)

.....Rv191T7.seq:.....

CGGTCCGACCCTGTTTCGACGGCTACCTGAATCAACCCGATGCCACCGCCGCGGCGTTCGACGCCGACAGCTGGTACCG
CACC GGCGAGCTCGCGGTGGTTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTCGGTTCGACTTGATCAAGTC
GGGTGGATACCGGGTCGGCGCCGGTGAAATTGAAACGGTGCTGCTCGGGCATCCGGACGTGGCGGAGGCGGCGAGTCGT
CGGGGTGCCCGACGATGATCTAGGCCAGCGGATCGTTGCCCTACGTAGTCGGCTCAGCGAATGTCGATGCGGACGGGCT
TATCAACTTTGTTGCCCAACAACCTTCGGTGCACAAGCGCCCGCGGAGGTGCGTATCGTANATGCGCTGCCGCGCAA
CGCCTTGGGGAAAGTGCTCCAGAACATTGCTGTCAGAAGCTGANCTACGCGAATTATCGTGTACGCTGGA

(SEQ ID NO. 183)

Clone Rv192

.....Rv192SP6.seq:.....

ATACTCAAGCTTGCCGAAGTTCCGATGGGTGCGCGCGGCGAGCCAGCGAAGTCGCTACCGTGGCCGTGTTCTTGGCT
TCGGATCTATCCTCGTTCATGACCGGCACCGTGTGGAGCTGACTGGCGGCCGGTCCATATGACACCGAGATCATTGC
CACGGTACGGCAATTCGTCAAGAAGGAAATCTTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA
AATCGTCGATCGGCTGGGTGTTATTGGCTTGCTCGGTGCGCGGCTGCAAGGGTATCGACACCGAGTTCATTCTCG
GGCGTGCCGGCGCATTTCGAGCTGGCGGTGCGCGCTGCCAGCACCCTCATAGGTACTTGACGATGGTCCACGTCGGAC
GAGCGCTCCACGTGCTGCCGAACGGTATGCATGGCGGCTACGATTCTC (SEQ ID NO. 184)

.....Rv192T7.seq:.....

CGGTGTCGGCACCGGCGTCTGTCAGTTGGTAGGCCTGCAGTTTGTGCATCAGGCCGATGCCGCGGCCCTCGTGGCCAC
GCATGTACAGCACCACGCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCTCCAGCTGAGGCCCGCAATCGCAGC
GGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGACCGAGCAGTCGTACCGTTCGGCGTTGGGCC
CGGCGATCTCGCCGCGGACCGCGGACATGTTCCACGTCCTCGTAGATGCTGGTGTAGCCGATGGCGCGAACTCCC
CATGACGAGTCGGAATCCGCGCCTCGGCGACCCGCTCAATGTGCTTCTCGTGCTTGGCGGCCATTTCGATCAAGTCAG
CAATGGTGATCAGCGCCAGACCGTGCTCATCGGCGAACACCGCAATTCATCGGTGTTGCGCCATCGAGCCCTCATCTT
TTTGGCTGACGATCTCGCAAATCGCCCCCGGGTTGCAGCCGGCAT (SEQ ID NO. 185)

Clone Rv193

.....Rv193SP6.seq:.....

ATACTCAAGCTTTGGGTGAAAGCCGATCACCGGAAGCCGCATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGG
CGTACCGATCTCCGCGTCATACACCGCGGGTAATCGCCGACGGTGCCGTTTCGCGAGCCGAAGGTGACGACGCTGAT
TGAATCGAGTTCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGTCAACGACGTCATACGTTGTGCTTTCTAC
GGTCACCGACCCGGTGACCGTNTCGCCCGGTGCGCTCGGCCGATAAGTTGCACCGCCACCACCGCGACACCGTCTTG
CACGCGGACCCACCCCGGATCCGTTGTTGGCC (SEQ ID NO. 186)

.....Rv193T7.seq:.....

AGCTTGCTGGCATCCGCTCCAGTAGCGCCCCGCGGTGGCTTCCAGCGCCCGCAGATGCTCCATGAGCCGGCCGGTCCG
AGTCGGCGCCGGCGTTACCCGCCACCCGCCAGGAGCTGGCGGCCAGCATCTCCGCCTTACGCAATTGCGCGATCACAG
AGAGAATATATCTCATATTCTGTTGGAGGTGCTGCGAGGCAATCGGTGATGACGATTGATGGCATCGAGCTGTG
CTTCGGCGTAGCCCTCCAGCACGTCGGTATCGCTGTGGCGGTCCACGACGACCGACCGGCGCGGCGGACAGCCGTCCG
GGTTGGACGNTGTGCGGCGATCAGTCCGGCCAGCTCCGCCTCGGGATCAGCGGC (SEQ ID NO. 187)

Clone Rv194

.....Rv194SP6.seq:.....

ATACTCAAGCTTGCTGCAGCTTCCTATGACTGCTCCCGAAACCTGGGGGTGTCCTGCTGTGTATGCACGGCATAACGG
ACATCCTTCCCTTGAGACCCGCGGTGCAACCAGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGACGGC
ACGCCAAGTTCGCCGACCGTTAACCTAGTGCTGTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTTCGGCCGTTAGGA
ACTGAATTGAAACTCAACCGATTTGGTGCCGCGTAGGTGTCTGGCTGCGGGTGCCTGTTGTCGCGGTGTGGT
AACNACNACAATGTACCGGGGGAGGTGCAACCACTGGCCAGGCGTCGGCGAAGGTGATTCGCGGGGGGAAGAAGAAC
TCAAAGCCAGTGGGTGACGCGCAGGCCAACGC (SEQ ID NO. 188)

.....Rv194T7.seq:.....

AGCTTGACGCGGAGACGGACACATTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAGTCACCGAGCCGA
TCAAGCCTTCGCCGAGCCAAATTCCAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGATTCCGTCA
TTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAACGGTTCGCCGTGACAGCAT
TAAATGTCACGGTATTGTAGATTAAGATACCCACCAACAAGGCAATCAAATGAGAGCGGTTAAATTGACCGTAA

AAGCGTCCGTCATCTGTTTGACGGTGTCCCGTTGGGTATCCGACGTTTCCATACGCACACCGGCCGCGCAGTCTTTGTT
GGATGCGTGTTCAGTGGCCTCATCTTTGATGATCAAATCGATGTGGCTCAGTCTTCCGGGCA

(SEQ ID NO. 189)

Clone Rv195

.....Rv195SP6.seq:.....

ATACTCAAGCTTCGGCTCAGGCGGCGTGCTGGTAAAGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTC
GGCGGCTACGTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTC
TTGAGCATGAGTCGGCGACCGTCGTCATGGTCGACACCCACGACGGAAGACGAGATCGCCGTCAAGCATGTGTGCC
GCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTCGCGATGCCTGGCGCCCGCGGCGGTGGTCGTGG
TCCGCTCGGATAGCGAGGTGAGCGAATTNCNTGGCAGCTCAAAGGGTCCTGCCGGTGCCGGTCTTTGCGCAAACNA
AGGCNCAGGTTA (SEQ ID NO. 190)

.....Rv195T7.seq:.....

TGATCGCGCATCACCTGCTTCATAAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCG
TCGGCGGTTCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCG
ACGAACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCCCG
GGTGTGGGGTGTTCGCGCAGCGCGCAGCCAGGTGGTCCACACTGCCGACGGGCGCCGCGAGCCGTTACCGACCGAGGC
CGCCGAGCAAGTCCGCCCGATCGCATACTCCAACCGGTTGCGGTACTGCAGGTTAGCTGGCGTACTCCTCGTCGCGC
TCGGCGAGGTCTTGCTCCAGCACGTCGCANACGGCAG (SEQ ID NO. 191)

Clone Rv196

.....Rv196SP6.seq:.....

CAAAGCGGAAGTCTCGCGGCAGCCACGACGTGCTGCGTCGGATTGCCGGCGGCGAAATCAATTCCAGGCAGCTCC
CGGACAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTACCCCGGTGCCCGGGGTCTGGTGCACCTGCCGA
TCGCACAGGTTGGCCCAACAACCGCCGCTTGATGCCCGGTGCGCAAGCCCGGCAGTTGCCAAACCCAGCGTGATCAGG
CTCGGCTCGCGAGTTCGGGAAGAAGTGGCTCCGCCTGATCACCTACCATCCGCCAGGATCTGCGTGTCTTCACCACG
CCCGCAAGGAGGTTGTTGTGGTGCTATCGACCGN (SEQ ID NO. 192)

.....Rv196T7.seq:.....

CCGGAAGCCGCATGATCAGCCAAGTTTCGCGCCGCGCCGGCATAACGGCGGCGTACCGATCTCCGCGTCATACACCCGCG
GGTAATCGCCGACGGTGCCGGTTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCAGGTCCAGCGGGTGGC
GCAGCAACGGCGCGAGCTCAACGACGTCAATCACGTTGTGCTTTCTACGGTCACCGACCCGGTGACCGTNGTCGCCC
GGTGCCTCGGCCGAAAANTTGCACCGCCACACCGCGAAACCGTCTTGACNCCGGAAGCCACCCCGATCCGTTGT
TGGGCCAGGTTATTGGGT (SEQ ID NO. 193)

Clone Rv19

.....Rv19SP6.seq:.....

CCGGAACCGCCGACGGCACGGTATAACGCCTCCGCATATGGGTGCAACAACAGCGGGTCGGACTTCTGGGCTTCTAGC
GTTTCGCGNGTCGCGACAAACAGCGCGGTGCAACCGACACTCGTTGTGATGTCCTAGCTATCAGGTTCCGGTACGCACC
CAATCGAGTCTAGCGCGGGTAGNTCAGCCCCGATCTCCANGCTCCGCCGAGCCAGGCGC (SEQ ID NO. 194)

.....Rv19T7.seq:.....

CTGGTTTATGTCCCGTTGAAGTTCCATCACCCGATGTGGCGGGAGCACTGCCAGGTGATCTCAACTACCACATCCGG
CCGTGGCGGTTGCGCGCCCCGGGGGTGCGCGCGAACTCGACGAGGCGGTGCGAGAAATCGCCAGCACCCCGCTGAAC
CGCGACCACCCGCTGTGGGAGATGTACTTCGTTGAGGGGCTTGCCAACCAACCGGATCGCGGTGGTTGCC

(SEQ ID NO. 195)

Clone Rv1

.....Rv1SP6D2.seq:.....

CCGAGCAGTTGGGAATCGCTCTGCANCAAACCAATATTCTGCGCGACGTCGCGCGACGAGCTGGACCGATTAGGCGTA
CGCCTCCGNTGGACGACACCGGGGCACTCGATGACCCCGACGCTACGCTCGCAGGATATTGTTGCGCCGACCCCTC
TCTAG (SEQ ID NO. 196)

.....Rv1T7.seq:.....

TATATAATACTCAAGCTTGCCGACGCCAACGCTCGCGCGATGTTGTTAGCCCGACCCGGCTCTTACATGGCACCGGTG
CCCCACACGTCAGCCTGTGACGTCCTGCACCGCGACTCTTTACATAGAATGTGGATTGCCGGATTGGGGATGTCCGGC
ATCGCTCAATCTGTAGTCCGCGTTGTCCCGCGAGGGCCATGTGGATGGGGGAAGGATCCGTGGCGTCCGGGATCACC
ATGGGG (SEQ ID NO. 197)

Clone Rv201

.....Rv201SP6.seq.....
ATACTCAAGCTTGCCGAAGTTCCGATGGGTGCGCCGGCGAGCCCCAACGAAATCGCTAGCGTGGCCGTGTTCTTGGCT
TCGGATCTATCCTCGTACATGACCGGCACCGTGTGGACGTGACTGGCGCCGGTTCATATGACACCGAGATCATTGC
CACGGTACGGAATTCGTCCAGAAGGAAATCTTTCCCAATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGA
AATCGCTAATCGGCTGGGTGTTATTGGCTTGCTCGGTGCGCGGTGCGAGGGTTCTACACCACCGAGTTTCATTCTCG
GGCGTGCCGGCGCATTCGAACCTGGCGGTGCGCGCTG (SEQ ID NO. 198)

.....Rv201T7.seq.....
GCACCGGCGTCTGCGAGTTGGTAGGCCTGCGATTTGTGCATCAGGCCGATGCCGCGGCCCTCGTGGCCACGCATGTAC
AGCACCGCGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGCGCTCCAGCTGAGGCCCGCAATCGCAGCGGCGTGAC
CCAAACACATCGCCGGTCAAGCACTCCGAATGCACCGGACAGCAGCTCTTACCCTCGGCGTTGGGCCCCGGCGATC
TCGCGCGGACCAACGCGACATGTTCCAGTCTCGTAGATGCTGGTGTAGCCGATGGCGCGAAACTCCCCANGACAA
GTCCGAATCCGCGCCTCGGCGAACCGCTCAATGTGCCTCTCGTGCTTGGCGCGCCATT (SEQ ID NO. 199)

Clone Rv204

.....Rv204SP6.seq.....
TGGTCCGTGTGCGCATACCAATACAACGCGCCGGGCACCTGACGCGCGGCCGCAACCAATCGGTGGCCATCGCCATC
TTCTGTACCCGGTCAACGGACGCACCTTCTCCTGGCCGACGTAGTGCGCCACCCGCGCCGTGCGTCCCATCGAT
CCGGTCAAC (SEQ ID NO. 200)

Clone Rv205

.....Rv205SP6.seq.....
GGCGTGTGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCC
GACTTTCGCGGTACCCGCTCACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACCTAC
TTCATCCTGACCGCGGAACAAATTGACGCGAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTAC
ATCATTCGCACGGAGAACCTGCCGCTGCTAAAGCCACTGGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCT
GGTTCAACCAAACTTGAAGGTGATTGTTTACCTGGGCTACGGCGACCCGGCCTATGGTTATTGCACTCCCCGCCAA
(SEQ ID NO. 201)

.....Rv205T7.seq.....
CGTCCGTGNNCCCTCAANCGCGTGNNGCCGAAGCGGCTGGTTACGACTCCCTGTTTGTGATGGACACTTCTACCAACT
GCCATGTTGGGGACGCCCCGACCGCGATGCTGGAGGCTACACGGCCCTTGGTGGCTGGCCACGGCGACCGANCG
GCTGCAACTGGGCGCGTTGGTGACCGCAATACCTACCGAGCCCGACCTGCTGGCAAAGATCATACCACGCTCGA
CGTGGTTAGCGCGGTCGAGCGATCCTCGGCATTGGAGCCGTTGGTTTGGAGCTGGAAACACCGCCAGCTCGGCTTCG
AGTTCGGCACTTTCAGTGACCGGTTCAACCGGCTCGAAGAGGCGCTACAGATCCTCCAGCCAATGGTCAAGGGTGAGC
GCCCAACGTTTTTTCGGCGATTGGTACACCACCGAATC (SEQ ID NO. 202)

Clone Rv207

.....Rv207SP6.seq.....
CCGCTTCCGTGTAACCGAGCANNGCAGCGANCTGGCGAGGAAGCAAAGAAGAACTGTTCTGTGATAGCTCTTACG
CTCAGCGCAAGAAGAAATATCCACCGTGGGAAAACTCCAGGTAGAGGTACACACGCGGATAGCCAATTCAGAGTAAT
AACTGTGATAATCAACCCTCATCAATGATGACGAATATCCCCGATATCAGGTCACATGACGAAGGGAAAGAGAAG
GAAATCAACTGTGACAACTGCCCTCAAATTTGGCTTCTTAAAAATTACAGTTCAAAAAGTATGAGAAAATCCATGC
AGGCTGAAGGAAACAGCAAACTGTGACAAATTACCCTCAGTAGGTGAGAACAAATGTGACGAACNCCCTCAAATCT
GTGACAGATAACCCTCAGACTATCCTGTGCTCATGGAAGTGATATCGCGGAAGGAAAATACGATNTGAGTCGTCTGGC
GGCTTTCTTTTTCTCAATGTATGAGAGCG (SEQ ID NO. 203)

Clone Rv209

.....Rv209SP6.seq.....
TGACACCCAACAGAGGGCACTTAAGATGGCAATGCGGCGCGCTACCTGCACGTTTTTCGCGATGTCAGAGGATGCCGAG
GGAGAACAAATGCGAGCACGGCGCTGACNTTGCTCACCCTTTGGCGGGCGGTGACATTGGTGGTGGTGGCGGCTGCN
AGGCCGANTCNAGGCCGAAGCATATAGCGCGGCGGACCGCATTTCTGTCTCGACCGCAAGCGCGACCTCAGCCGACG
CGGTGGAGCTACTGCTGCGCGCCATCAGCC (SEQ ID NO. 204)

.....Rv209T7.seq.....
ACGGGCGACGCTGAGGTGGGCGCGGCTATTGCTGTGCTCCACGTCCAGCGACGCACTGCGCCAGACGGCCCGC
CAACTAGCCACCTGGGTGGAAGAACACAGGACTGCGTGGCGGCGCTCGGATCTGGCCTACAGCTGGCGCGTGGCCGC
GCGCACCGGCGGTGCGCACCGCGGTGGTTGCCGCCAACCTGCCGAGCTCGTCGAGGGTTTGGCGGAGGTGGCCGAC

GGTGACCCCTCTATGACGCGCGGTGGGACACTGTGATCTAAGACCGGTCTGGGTCTTCTCCGGGCAAGGGTCTCAGT
GGGCGGCGATGGGCACCCAATTGCTCGCCAGCGAACCAGTGTTCGCGGCCACCATCG (SEQ ID NO. 205)

Clone Rv20

.....Rv20SP6.seq.....
ATACTCAAGCTTCGCGAGATCCGGATGGCACTCACGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATAC
TTGAACCTGGTCTCGTTCGCAATAACTCGTTCGGCGTGCAGGACGCGGCGCAAACGTACTTCGGCATCAACGCGTCC
GACCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGAATCGACCAGCAGCTCAACCCGTACACCAACCCC
GACGCGCGCTGGCCCGGGAACGTGGTCTCGACACCATGATCNAAACTTCCCAGGGAGGCGGAGGCGTTGCGTG
CCGCCCAGGGCGAACCCTGGGGTTCTGCCGACGCCAATGATTGCCGCGCGGCTGCATCGCGGCGGCGACCGCCA
TTCTTCTGCGAATACGTCCAGGAGTACTGTCTCGGGGC (SEQ ID NO. 206)

.....Rv20T7.seq.....
AGCTTATGTGGCGCCACCTACCTTATCTAGCCTAGCTAACTAAATCCAGTGCCGACAGTGCGCGGCTGGCCACCCA
GCATGAGGTTATGACCACGGCATATGCCAGCGCGCTGGCGCGATGCCGACGCTGACCGAGTTGGCCGCTAATCACAC
CAGCCATGCGGTGTTGCTGGGAACGAATTTCTTGAATCAATACGATCCCGATCGCGCTCAATGAGGCCGACTATGC
GCGGATGTGGATTAGGCGGCCACACGATGAGTATCTATGAGGGCACCTCCGATGCGGCGCTGGCGTCNGACCGCA
AACCACACCGGCTCCGGTACTGTTCAACGGCGGTGCTGGCGTTGCCAGCGCCTGCCGGCGATCTC
(SEQ ID NO. 207)

Clone Rv214

.....Rv214SP6.seq.....
ATACTCAAGCTTGCCACCATGCCGAGCAAGGTCGACTCAGCGATGACGAATTGTTCTTCTTCGCGGTGTTGCTGCTG
GTTGCGGGCTATGAGAGCACTGCTCATATGATTAGCACNTTGTCTTCTGACGCTGGCCGACTATCCAGATCAGCTGACA
CTCCTTGCGCAGCAACCAGACCTGATCCCGTCGGCGATCGAGGAGCACCTCCGCTTTATATCGCAATCCAAACATCT
GCCGCACAACGCGCTCGACTATTGCTCGGTCAAGCGGTTCATCCCGGA (SEQ ID NO. 208)

.....Rv214T7.seq.....
CCGGGGTAGAACGATGCGATCTGGGCCATGTCGACATCGGTGGTACAGGTAAACCGCGCCGTGTGCGCGGTCTCGGAG
ATCAGAACGTGGTCGAGTTGACACCGCGGGCTTTCAGCCAGTCGCGATAATCGGCGAAGTCGGCGCCTGCCGCCCCA
ACTAGCGCGACCTCGCCACCTAGCACACCGATGGCGAAGGCCATGTTCCGGCCACGCCCGCGGTGCATCATCAAC
TC (SEQ ID NO. 209)

Clone Rv215

.....Rv215SP6.seq.....
ATACTCAAGCTTGCGGCAACGCCACTACCGGGCTCACCAGGTCTGTGCCGCCACCGCCGGCGCGGAAAGCACCATC
AGGTGCTAGTTGTCTGGACGTTGACACCGTAAGCGAACACAATGCCCGCGCCATGCTGTGCCCGAGCAGATGCGC
TTGCACCCGGGATATTCCCGGTGGCGATCCCAACGAGGGTGTGGAAGTCAGCGGTGTATCTGAGATGTCTCTACTA
TCATCCGTTTGGCACCCGAGCGGGCATGCCCGCGGGGGTCAAC (SEQ ID NO. 210)

.....Rv215T7.seq.....
GTGACGGCATCAAGTCCGCGATGATGGTGTTCATCTCACCAGGAAGGCGTGAAGTGGCTGATACCGTGGCTTGAG
GATTCGGTGCGGGTCGCCAGTTAATCCGCCGTGTGCTCCGGATGAGCGCGACGGTAACCTGGAATTGTGCTGTGTGC
TGGCTGTGTCGTTGTGATGAGCCTGTCTAAGTGGTGCCTAACGTTTGACGAGCCGCGGCTCGCTGCAAACATTGAA
GCCCCACGCTCTGGGTTTGTATTTACACAACGAGGGCGCTCCCCGATCTGGCGCGCGCAACGAGGTGCNCACTATCCA
TTCGAGGTGAACTGGACTCCTTGATGCTCATGCCGGTGGCGTTTGTGTC (SEQ ID NO. 211)

Clone Rv217

.....Rv217SP6.seq.....
ATACTCAAGCTTGCGTTCGATGAAGTAGTCTCGGTGACGCGCCGCTCTTCGAGCTCCTTGCGGATGCCAGCAAGGA
GTCATCGCCGCGAGCTTGCCAGGATCTTGTGCGCCTGTTCTTGACGATGCGGGCCCGGATCGTAGTTCTTGTA
GACACGATGACCGAAACCATCAATTTGACCCCGGCTCGCGGTTCTTGACCTTGCGTTACAACTCGCTGACGTCGT
CGCCGCTGTGCGAATGCCCTC (SEQ ID NO. 212)

.....Rv217T7.seq.....
NGTCAAGCCGAGCATGCGCGAGGNAACGACGAACCAACAAGCCATGGTGGTTGGCGCCGTCGAGAGGTGCGCGGTGCG
CCACAACGGGAAGATCGCCTTGAGCGTCGCTCGACCGCCGCTCGAGTTGGGTGATAACGAAGTAGCTGATGCCGATC
ATGTCGACGTTTCCGTGCGATCAGCGTGCAGCGCGACCCACTCGACGAGGTCTCGGTGCCCGCGCGGCCAGGGCACC
AGCAGTGACGATTCAGGCGCGGTGCGG (SEQ ID NO. 213)

Clone Rv218

.....Rv218SP6.seq.....
CGATAATCGCTTCCGGTAAGTGCAGCAGCTTTACGACGGCGACTCCCATCGGCAATTTCTATGACACCAGATACTCTT
CGACCGAACGCCGGTGTCTGTTGACCAGTCAGTAGAAAAGAAGGGATGAGATCTCCCCGTGCGTCCTCAGTAAGCAGC
TCCTGGTTCGCGTTCATTACCTGACCATACCCGAGAGGTCTTCTCAACACTATCACCCCGGAGCACTTCTAGAGTAAAC
TTCCCATCCCGACCACATATAGGCTAAGGTAATGGGCATTACCGCGAGCCATTACTCCTACGCGCGCAATTAACGAAT
CCACCATCGGGGCCGCTGGTGTCTN (SEQ ID NO. 214)

Clone Rv219

.....Rv219SP6.seq.....
NAATACTCAAGCTTTCTCGTGATTACCAACCCGTGTAATTTGGGATGGGCAAAAAGGCGAATCACCGCGTGGCCACAAA
CGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTCCGCGTC
GCCCTCCGACCGCGAACATTTCGGGGATGGCAGCAACCTGGTATCACCTGGCCGGGCAATGATCTGCAGCGTCGCCGC
GGGTAGTGNCCGCCCGGGCGGCTAC (SEQ ID NO. 215)

.....Rv219T7.seq.....
CCAAGTACGAGCATCGGGACATACGAGTCAACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACG
ACGCCAGCGACCACATTCAGCAGATGGCCAGCGCGTGCCGGGCCACGATGTTGGTGTCTCGGCGGCTACTCCAGGGTG
CGGCCGTGATCGACATCGTCAACGCCGACCACTGCCCGGTCTCGGGTTCACGCAGCCGTTGCCGCCGCGAGCGGACG
ATCACATCGCCGCGATCGCCCTGTTCCGGGAATCCCTCGGGGCCGCGCTGGCGGGCTGATGATCGCCCTGACCCCTCAA
TTCGGGTCCAAGA (SEQ ID NO. 216)

Clone Rv21

.....Rv21SP6.seq.....
ATACTCAAGCTTGCTGCAGCTTCTGTGACTGCTCCCGAAACCTGGGGGTGTGCCTGCTGTATGCACGGCATAACGG
ACATCCTTCCCCTGAGACCCGCGGTGCAACCAGCCACGTGTCCATCATCAGGGGTCAACCCCGGCCAAGGGCGACGGC
ACGCCAAGTTCGCCGACCGTTAACCTAGTGCTGTTAGCTTCATTTGCTGCGAGCAAAACAGCTGGTTCGGCCGTTAGGA
ACTGAATTGAAACTCAACCGATTGTTGGTGCCGCCCGTAAGTGTCTGGCTGCCGGTGCCTGGTGT (SEQ ID NO. 217)

.....Rv21T7.seq.....
AGCTTGCGCGGCGTGGCGATCGCGGTTCAAGGCGCGCTCTTCGAGCACAAACGAGCGAAGACAGCTCGGCGACGGAGCC
TTTATCGACATCCGTTTCGGGCTGGCTGACCGGCGGCGAAGAACTGCTGGACGCGTTGTTGTGACGGTGCCGTGGCGA
GCCGAGCGCCGTGATGTACGACCGGGTGGTGGATGTGCCGCGGCTGGTGAGTTTTCACGACCTGACCATCGAAGAT
CCGCCGCATCCGCAGCTGGCGCGGATGCGCC (SEQ ID NO. 218)

Clone Rv220

.....Rv220SP6.seq.....
AATACTCAAGCTTGCGCACGACCAGGACGTGAGTGGCGCTTGCACTGACTTGGCGACCTCAAAGGCCACCGGTACCC
CGCCGCGCGGCAAGCCAAGGACNACNACGGCCTTGCCGATAGCTGCGCCAGGCGTTGCGCCAAGTGGCGTCCAGCGT
CGCCACGATCGTCAAAGAGCTTCATCTGCCGAGTGTGTCGCCATCTCATGGCTCCAAATATGGAATTAGGTCCCTGGG
CCGACTGACGACAGTCCCTCAGCGACCGGATTGCGCATCCCGCCTTGACGCTGCTCCGCAAATCCCGGGCTTGCGTC
CGCGGAAGCGAACTCGGCGGCGCTACGGTGGTGGTCACTTCGGCCGTGC (SEQ ID NO. 219)

.....Rv220T7.seq.....
GGTTGGTGCGGTCCACCTTCGCGGCGGCGCGGATATGCCTTGCTGGTCTTGCTCATTTGATATCCAATCTATGGGT
CGTGGTTACTCAGCGGGCCGAAGCTGGCCCTCCACCGGTAGGGCCCTATTGACGGTGATGCCCATCGACCGAGCGG
TACCGGCGATGATCTTGGCCGACGCTGACGCTGCTTGGCGTTGAGGTCCGTCTTCTTGGTCTCGGCCGATTTGCGGGA
CTTGATCCCAGGTGACTTTGGCGACCTTGGTCTTGTGCGGCTCCGCCGAACCCCTTCGCCACACCAGCGGCCCTTAAGCA
GCAGCTTGGCGGCGGGCGGCGCTTTCAGCGTGAAGTGAAGCTACGGTCTTCATAAACGGTGATCTCCACCGGGATGA
CGTTGCCGCGCTGGTTCTCCGTGCGGCGGTTGTACGCCTTGCAAGTCCATGATGTTGACCCGTGCTGACCGAACGC
GGGGCCCACTGGCGGGGC (SEQ ID NO. 220)

Clone Rv221

.....Rv221SP6.seq.....
ATACTCAAGCTTTTCGACCCGCAAGCCGGCGGTGCCCTCCTCGTTCCGCTGCCCGGTCTGCTCGATCGGTTCCGGGT
CGCCGCGCTAGGCCCAATTGCCCCGCTCCTCCTCGGGCGGTTCCACAACCCGCATCGTCGCCGGGCTAGGTTCAAGCC
ATGCCGGTAAACCCAGGACGCCAGTGCTGATCGGCTATGGACAGGTCAACCACCGAGGCGACATCGACGCCNAAAT

CAGTCCATCGAACCCGTCGACCTGATGGCCNCCGCGGCCCGGAAAGCCGCCGAGTCCACCGTGCTCGAAGCGGTGGAT
TCCATCCGTGTGGTGCACATGCTGTCGGCGCATTACCGGAATCCCGGGCGTCTCCTCGGC (SEQ ID NO. 221)

:::::::::::::Rv221T7.seq:::::::::::::
NCCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGTTCGGG
TGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACGAAACGACGCC
AGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGGTTCTCCACCGACCGGGCCGGGTGTTGGGGTG
TTCGGCAACGCAACCAAGTTGGTCCACACTGCCGACGGGCGCCGAAATCCGTTACCCGAACAGGCCGCCNAAACA
ATTCCGCCCGATCCCATAT (SEQ ID NO. 222)

Clone Rv222

:::::::::::::Rv222SP6.seq:::::::::::::
ATACTCAAGCTTGTTCGGGATCAATCTCGAGGGCATCCACGCAGAAAAGTAAACTCTATCAAGCTTTTTCAGCACACC
CACGGACGCCCATATATGTTTCGGGTGGGCAAGAACGGTCCCTACCTGGAACGTTTGGTGGCCGCGACCCGGTGAG
CCCACGCCGACGCGGGCCAACTCAGCGACTCGATTACCCCGGACGAACTGACTCTACAGGTGGCCGAAGAGCTCTTT
GCCACACCGCAACAGGGACGGACTTTGGGCTTGGACCCAGAAACCGGCCACGAAATCTTTCAGGGGAAGGCCGGTT
TGGGCCTTATGTTACCTATATCCTGCCGAACCTGCGGCTGATGCGGCCGCGGCCGCTCAGGGAN (SEQ ID NO. 223)

:::::::::::::Rv222T7.seq:::::::::::::
AGCAGCTAGCCGCGCTCGCCGCGCTGGTTCGGTGCATGCTCGCAGCCGGATGCACCAACGTGGTCGACGGGACCG
CCGTGGCTGCCGACAAATCCGGACCACTGCATCAGGATCCGATACCGGTTTCAGCGCTTGAAGGGCTGCTTCTCGACT
TGAGCCAGATCAATGCCGCGCTGGGTGCGACATCGATGAAGGTGTGGTTCAACGCCAAGGCAATGTGGGACTGGAGCA
AGAGCGTGGCCGACAAGAATTGCCTGGGTATCGACGGTCCAGCACAGGAAAAGGTCTATGCCGGCACCGGGTGGACC
GCTATGCGCGGCCAACGGCTGGATGACAGCATCGATGACTCCAAGAAACGCGACCACTACGCCATTCAAGCGGTGCTC
GGCTTCCCGACCGCACATGATGCCGAAGAATTCTACAGCTCCTCCG (SEQ ID NO. 224)

Clone Rv223

:::::::::::::Rv223IS1081N1400.seq:::::::::::::
CGCGACTGGCTCCCCGNGCGCTGCTCGGGTCCGCCGATAGAGACCGGGATGTCGCCCCGACGACGGGCAGCCGGGTG
CGTGGGACGGGGCGGGGTTCGGGCAGCCCAAGCAACGGGCTAGTCCCCGAATCCTACGGAGCCGTCACCTACGCCTAC
GTAATAGTAGCTATCAATAACAGTTGACATACGCAACGATCTGTGAGATCAATATTGCCTGACGCATGTCAAGACAGG
CGTCAAGACAGGTGTCAATAATTGCTCCGCTGGTGACGGTAACGGTTCGTGCGGGTGTGTGACGCCTAAGGAAGGAG
TGTGGGTGGTGACGCTGAGAGTGGTTCTGAGGGTTTGGCGGCCGCCAGTGCGGGCGGTGGAGGCGTTGACCGCACGGC
TGGCCGCGGCACACGCTGGCGCGCGCGCGGATTACGGCGGTGGTGGCGCCCCGCGCGGATCCGGTGTGCTGTCAGA
ATGCGGTGGGGTTTAGCGCCTTAAGTAGCCAGCATGCCGCGATCGCCGGCGAAAGGGTCCAAGAACTGGGT
(SEQ ID NO. 225)

:::::::::::::Rv223SP6.seq:::::::::::::
ATACTCAAGCTTATTGAACCGCGGGTTCGACGCAAAAGTGGACCTCATAACGACTCGGGTCCAGCGACCGCGCCAACAC
GAACGGCCGGACGACGTGGGCCAGGGTCGCGGCCTCCCTACAAACAGGATCCGTTGCCTGCGAACGACAGGCTCCGG
TGCGGCGTTGGGCGCGCTGCTCGTCCCAGCGTCCGGTCCCGGGTTCGCGGCGACGCTTGTTCCTCCATACTCGCCCC
CTAATCTCGAGGCAGCCCGTACCCGCGAGGCAACCTCCCAAAATGCAATCCCGCAAAATGCAATGCGTCNAGCTATTT
CTCACACCGACCGCTAGTTGCGGATCAGAAATCCGTTGGGCGCGGAAGTCCAGCCGAATTTGTTCTCCCGCTCCGCAT
CATGCTTGTAATCGTTTGGAAATTCATCCTCATATGCCTCGATCGCTTCATAGGGTCCAGGCCCAAACCGGGCGAGGA
CTGGGTGGCCGTTGATGTTGGAATCCTCCACTACTAGGTATTCACCGGC (SEQ ID NO. 226)

:::::::::::::Rv223T7.seq:::::::::::::
GTCTCGATCATGGCCAAAGAGCTCGACGAAGCCGTAGAGGCGTTTCGGACCCGCCCCGCTCGATGCCGGCCCGTATACC
TTCTTCGCCCGCCGACGCCCTGGTGTCTAAGGTGCGCGAGGCGCGCTCGTTCGGGGTGACACCTTGATCGCCACC
GGCGTCAACGCCGAGGGCTACCGAGAGATCCTGGGCATCCAGGTACCTCCGCCGAGGACGGGCGGGTGGCTGGCG
TTCTTCCGCGACCTGGTTCGCCCCGCGGCTGTCCGGGGTTCGCGCTGGTACCGGCGACGCCCACGCCGCGCTGGTGGCC
GCGATCGGCGCCACCTTGCCCGCAGCGGCTGGCAGCGCTGCAGAACCCTACGACGCAATCTGATGGCAGCCACC
CCGAAGCCCTCCTGGCGTGGGTGCGCACCTGCTGCACTCCATCTACGACGACCCGACGCCGAATCAGTTGTTGCC
AATATGATCGGGTTCTCGAC (SEQ ID NO. 227)

Clone Rv224

:::::::::::::Rv224SP6.seq:::::::::::::
ATACTCAAGCTTTCGTGAGTTCATGGCGCCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCA
ACGGTGATTTCTTGGCCGCCGCTGACGGCGCAACGACGCCAGCGACCAATCAGCAAATGGCCAGCGCGTGCCGGG

CCACGAGGTTGGTGCTCGGCGGCTACTCCCAGGGTGCGGCCGTGATCAAGATCTTCACCGCCGCACCACTGCCCCGCC
TCGGGTTACGCATCCGTTTGGCCGCCGCC (SEQ ID NO. 228)

.....Rv224T7.seq:.....
GCCCCGTGTAATTTGGGATGGGCAAAAAGCGAAGCACCGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCT
AGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCAACATTCCGGGAT
GGCAGCAACCTGGTAGCACCCCTGGCCGGGCGATGATCTGCAGCGTCGCCGGGGTAGTCTCCGCCCCGGCCGC
(SEQ ID NO. 229)

Clone Rv225

.....Rv225SP6.seq:.....
ATACTCAAGCTTCTTTGACCGAACCGCTCCACCGCACCGTGAGATTGGTGGCGCCATTCTGTCGTGGTGTAGCTGCTG
TTGGCGGCGTCGCCGATTGTGCGGGCCAGCCTTGTGCGGGGGCCGCTTCTACCCACAAGTCGGCACTTCCGCAACCG
CCCAGCTCGACCGCGAATTACGGCGGCCGCAACGGCCGCCGAAGGCGTCACGCAATCGCTTATCCTTTCCAGGTTCC
CAAATCCTCCGCTTACTTGGGTCTTCATCGG (SEQ ID NO. 230)

.....Rv225T7.seq:.....
GGCAGCGGCGACAACCGGAACGTCCGCGACGGTGCTCAATCACGGGTGCACGGTGTGCATCAGAATGGCGGGGGTTCGT
TGTCGCGGTGAGGCGTTCCGGCAGGAGGTAGTGTCTACCCCTTGCCCGCGGGTTCGTGCGGACTGAAAGGGATTTCTAT
TGGGAACCCACGGCTGCGTATCGCAGGGCCTCGGTGACGTCTGCTTCTCNAGCTCAGGAAGTTCGGCGAGAATCTCG
GTGGATGTTATTTGGTCCGCCTAC (SEQ ID NO. 231)

Clone Rv226

.....Rv226SP6.seq:.....
ATACTCAAGCTTTCTCGGCTTCTCTGATAGCCTGAGAAGAAACCCCAAGTTAATCCGCTGCTTCACCTATTCTCCAGC
GCCGGTTATTTTCTCGCTTCCGGGCTGTCATCATTAACTGTGCAATGGCGATAGCCTTCGTCAATTCATGACCAG
CGTTTATGCACTGGTTAAGTGTTCATGAGTTTCAATCTGAACATCCTTTATTATTGTTTTGCGTT
(SEQ ID NO. 232)

Clone Rv227

.....Rv227SP6.seq:.....
ATACTCAAGCTTGGTGACCGGCACCGCGATACGTTGCGGCAGGCATCTGGGCTGGCGGTGGTTCCGCCGCTCCGAAGCC
GTGGAACACCATCGCCAGCGCGGCTTCCACATCAACGACCATTTCCGCCAGCTTGCGGCGCATCAGCGGCTTGTCGAT
GAGCGCCCCACCGAATGCCCGCGCTGCCCGGCGTATCACATCGATTGACCATCGCGCGGCGCGGCTTGCCGAGGGC
GAACGAGGCGGTGCCCAACCGCAATCTGTTTGGTCAGCTCCCTCATCGGGTTGATTCCTTGCCGTCGGGACGGGCCC
CGGTATGCGCTCGGTTCCGC (SEQ ID NO. 233)

.....Rv227T7.seq:.....
CCGTTGCGCAGCGTGAGCCGATAGTTGACATCCGGCTCGGTGAAGGTGAAATCGATGGCCAGGTGAGGTCCCATGCG
CGTGGGCCATTGATGCTGATCGCCAGGACGTCAAAGATTTGGTCCGGCGTCAGCTGGGCGAAAAACGTGGGCGCCGGG
ACTTGCCCGGAGCTGCCCGGGTTCCCGTCGCGCAGCTCGGCGGCCCCGGTCAGAAAGAAATTGCGCCAGGTGCGCACAC
TCCGCGCGGTAGGCCAGCTGCTCCAGGGTGTGCGCATAGAGCCCGGGCCGACGCGTGTGCTGTCGGCGAACACC
GCATGGTCGAGAAGCGTTGCCGCCAACGGGAAATCACCTGCGTCGAAAGCTTCGCGGGCCAGCTCCAGCACTCGGTC
GATGCCACCCAACGCGT (SEQ ID NO. 234)

Clone Rv228

.....Rv228SP6.seq:.....
ATACTCAAGCTTGGCGATGTTACCCCTGACAGCGTGAACATATGTCNAAACACACGGCACCGGAACGGTGTGGGGGAC
CCCATCGAGTTCGAGTCGCTGGCGGCCACTTATGGCCTGGGTAAGGCCAGGGCGAGAGCCCGTGGCGATTGGGGTCCG
GTCAAACCAACATCGGCCACCTGGAGGCGGCCCGCGGTGTGGCTGGATTATCAAGGCGGTGCTGGCGGTGCAACGT
GGGCACATTTCCCGCAACTTGCACTTACCCGGTGGAACCCGGCCATCAACACGTGCGCGACGCGGCTGTTCTGTGCCG
ACCGAAAGCGCCCCGTGGCCGGCGGCTGCCGGTCCACGCAGGGTGCAGGTGTCATCGTTCGGCCTCAGCGGGACCAA
(SEQ ID NO. 235)

.....Rv228T7.seq:.....
CCGGTAACCAGATCAGCTCGTCGACCTACTGCCGGGGGTGAATTCCCCACCGGTGCTGCGCGCTGCCAGTAGTGCA
CCTTCTTGACGCTCGAAAAGGGGAGTCGGTCCGGTAGGTCAACGTCAGGAGCCGCTACCCAGGTTGGCGCGGTGAC
CGGTCTCCTCGAGTATCTCCCGCACCGCCCCACCGTCCGGTCTCGCCCGATCCACTTTGCCCTTGGGCAGCGACC
AGTCGTGTAACGGGGGCGGTGAATGACAGCGATCTCGACCGGCCCTTCCGAATCGGCACTGCCGGGTGCCGAGAACA
CCGCACCGGCGGCGTACACAATCCGGCCCGGAGCGCCGGCGGCGGACGANTTCTGGATCGACACCTCAACTCCTG
CAGGTCAATTCGGCCAAGCTGCTCGCGGTGCTGGATGTGGTC (SEQ ID NO. 236)

Clone Rv229

:Rv229SP6.seq::

ATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCACCCACCACGCGGGGTGGGGCGCCGGGCGCCG
GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCAGCGACACCACCGGCTGCGCTACGTGAGCCATACCGGGCG
GAGCTACATCGGCTCGGCCGCCAGTGTTGGGCCCTCTTCGAGGTCGAGGCTATACCGATTGCGCATCCGCAGC
CGACCCCTGGTCTGCTACCGTGCCCTACCTCTGCTTGTGGGGCGGGGCCA (SEQ ID NO. 237)

:Rv229T7.seq::

TCCGTACGGCCCGGGTACGCTTCGGTCGCGAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTCCATA
GCCCCGCACACCTTCAGTTGCTCACCGGAATCCAACCGGTAGAAGGTGCGCGAGCGCTCGGCATTGGTCATCGGGATA
TGCCGCTCGGGACGGTCAGAGCCCTCGGTCCGGCCAGCACTCCGCAGGCTTCGTGGGGTGGTCGCGACGCGCATGG
GCCACCATCCATCCACCAGGTCTGCGCAATCACCCGC (SEQ ID NO. 238)

Clone Rv22

:Rv22SP6.seq::

GGACACATTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAAGTACCAGGCCGATCAAGCCTTCGCCGAG
CCAAATTCCAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGATTCCGTTCATTATCAGCCAAAATAA
CTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAACGGTCGCCGTTGCACGACATTAAATGTCACGGTATT
GTAAATTAAAAAGATACCCACCAACAAGGCAATCAAATGAGAGCGGTTAAATTGACCGTAAAAGCGTCCGTCATCTG
TTTGACGGTGTCCCGTTGGGTNTCCGACGTTTCCATACGCACACCGGCCCGGAGTCTTTGTTGGATGCGTGTGCAAT
GGCCTCATCTTTGATGATCA (SEQ ID NO. 239)

:Rv22T7.seq::

GCCTGGCCAGGTGAAGGCCGACCTCGACGCCAAAGCCGCTGATCCGGCACATGAGTCGGTGGACTGGGACTTGAAGT
CGCTGCGATGGGCGTGGAACCGAGCCAAAGATGACGTGGCGCCGTGGTGGGCCGAGAATTCCAAGGAGTGCTACTCGT
CGGGGTTGGCCGATCTGCCCCAGGGCTGGCTAATTGGAAGCTGGCAAGAACGGGACCCGCAAGGCCGGCGGGTGG
GCTTCCCGCGATTCAAATCCGGGCCGGCGTGATCTGGCAGGGTGCGGTTCAACACCGGCACCATGCGCATAGAGGATG
ACCGGCGCACGATCACGGTCCCGGTGATCGGGCCGCTGCGGGCCAAGGAGAACACCCGCCGGGTGCAACGCCACCTCG
TGAGCGGGCGCGCAGATCCTGAACATGACCTTGTGCGAGCGGTGGGG (SEQ ID NO. 240)

Clone Rv230

:Rv230SP6.seq::

TAAGCTCAAGCTTCAAGTCCGCGTCCGACCTGTTGCGAGCGCTACCTGAATCAACCCGATGCCCGCCGCGGCGGTTCCG
ACCCGACAGCTGGTACCGCACCGGCGACGTCGCGGTGGTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTC
GGTCGACTTGATCAAGTCGGGTGGATACCGGGTCGGCGCCGGTGAATTTGAAACGGTGCTGCTCGGGCATCCGGACGT
GGCGGANGCGCGAGTCGTCGGGGTGCTCGACTATTATCTAGGCCAGCGGATCGTTGCCTACGTAGTCGGCTCAGCGAA
TGTCGATGCGGACGGGCTTATCAACTTTGTTGCCCAACAACCTT (SEQ ID NO. 241)

:Rv230T7.seq::

CCATGTCGCCCAACATATCGTCGATGTTGCGCTCGTCCGCTCGCGCACGTGGTCTGTACACAGTCAACGTTAACGCC
GCCGCACATGTCCTGCGGCCGGGCAAAAACGTGAAAAACGAGCGGGCGACTGCAATGTCATGACACCGACGCCGCCGA
TGGGCCAGGGTCTGGCAGATTGATCTGTGCGGCCAGTGCCAGCAGCGTCGCCTCGTCATACGGCCGGCCGACGAGT
TGAACCGACATGGGCATGCCGTGCGCGTGAAGTCCACGGCACCCAGGCCGCGGGCTGGCCGGTCAGATTCCANACT
TGAAAGTACTGAAGCCGCTGCACCACG (SEQ ID NO. 242)

Clone Rv231

:Rv231SP6.seq::

CGAAAGCGTGAAACAGCTCGCGGCAGCCCCGACGTGCTGCGTCGGATAGCCGGCGGGCGAAGATCAATTCCAGGCAG
CTCCCGGACAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTCAACCCGGTGCCCGGGTCTGGTGCACCTG
CCGATCGCACAGGTTGGCCACAACCGGCCGCTTGATGCCCGTCGGCAAGCCCGGAGTTGCCAAACCCAGCGTGAT
CNTGCTCNGCTCTNTANTTCGGCGAAGAAGTGGCTCGCCTGATACCTACCATCGGCCAGGATCTGCGTGTATCACA
ACGCTCGCCAAGGAGGTTGTTGTG (SEQ ID NO. 243)

:Rv231T7.seq::

TCCGCCACGCTTCGCGCCGCCCGGCATACGGCGCGTACCGATCTCCGCTCATACACCGCGGGTAATCGCCGACGGTG
CCGGTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCAGGTCCAGCGGGTGGCGCAGCAACGGCGCGAGC
TCAACGACGTCAATCACGTTGTGCTTTCTACGGTCACCGACCCGGTGACCGTAGTCGCCCGGTGCGCTCGGCCGAGA
AGCTGCACCGCCACACCGCGACACCGTCTTGACGCGGACCCACCCGGATCGGTTGTTGGCCAAGGTAATTGGGTC
ATTCCATTGACGGGACGCCGACCC (SEQ ID NO. 244)

Clone Rv232

.....Rv232SP6.seq:.....
CATTCTTTAACAGTTGTTTTGGGCTCGGCATGGTTAGCCAACGTTCTGCGGTCCACCATATCATCTTGGTCCGGTAGC
GTCGTCCGGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACCGCCACCGGTCCAGCGCGTG
GGCCGNCGGTCCCATCAAACTGAACCCCCAACAGGGACATGCTTATCGGTAGGGCGCGGCCAAGGCGGCAGCA
ATCGCATCACTGCGCTCTGCGCGTCACTATTAACCCACCCGGACTTCACTTCCACCACCCCGAATGGCGCCCGGTCT
TGATCATCTGGCGCACCGCGGATAA (SEQ ID NO. 245)

.....Rv232T7.seq:.....
CGGTGTCCTGCAGTTGGTAGGCCTGCAGTTTGTGCATCATGCCGATGCCGCGGCCTCGTGGCCACGCATGTACAGCAC
CACGCCGCGCCCTCACGGGCGAACATCGCCAGCGCGGCTCCAGCTGAAGCCCGCAATCGCAGCGGCGTGACCAAAC
ACATCGCCGGTCAAGCACTCCGAATGCACCGGACCAGCACGTGTCACCGTCGGCGTTGGGCCCCGGCGATCTCGCCGC
GGACCATGCGCGACATGTTCCACGTCCTCGTANATGCTGGTGTAGCCGATGGCGCGAACTCCCCATGACGAGTCGGA
ATCCGCGCTCGGCGACCCGCTCAATGTGCT (SEQ ID NO. 246)

Clone Rv233

.....Rv233SP6.seq:.....
CGGCATCTGGCGGCTGAACCTGTTCTTGGGCAACATGCCGAGGATCGCCTCTTCCACCACGCGGTGGGGTGGCGTTG
CATTACCTACCGATGGTGCCTTGTGCAGGCCGCGGGGATAACCCGAGTGCCGGTAAACCATCTTGTGCTGCAGTTT
GTCGCGCTGATGGCGACCTTGTGCGCGTTGATCACGATNACNAATACCCGCCANCGACATTGGGGGCGAACGTCGGC
TCGTGCTTGCCGCGCAGCAGGCTGGCCGCGCGACGCAAGGCGCCAACCACCACGTCCGTGGCGTCGATGACGTACCA
CCATCGCGTGGTGTACCCGCTTGGGC (SEQ ID NO. 247)

.....Rv233T7.seq:.....
GCGGCAAAAATTGAAGCACTCNTGGCCACTNCCGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGG
CCCGAACGTACTGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTCTGGGATGGCAGCAACCTGTTAGCAC
CCTGGCCGGGCGATGATCTGCAGCGTCGCGCGGGTAGTCGCCCCGGGCGGCTACAGTCTGAAACGCGATGACCATC
GATGTGTGGACGCCGATCCGACNCAACGGTTCCTACACTGTGATATGTTGCGCTCGCTGCGCCGGTGGACGGTGGGT
CTATCCCGGA (SEQ ID NO. 248)

Clone Rv234

.....Rv234SP6.seq:.....
CGCGTTGAACTGAAGGGGTGCCGCCGGCTCGAGCAGGCAAGCCATTTGTTGATGCGGTTACCGAAGATCTCTTCGG
TGACTGCCCCGCCGCGGCCAGCTCGGCTCAGTGTCGGCGTTGGTTCGCCGCGGCGACAATCTTGGCGTCCACGGTGGT
CGGGGTCATGCCCGCGAGCAGGATTGGCGAGCGGNCGGTCAGCCGGGTGAACCTTCGTCAAGAGCTGACGCTGCGGTTG
GGGAGCGCAATCATGGTCGGTGCCTAGCCTCGACTAGGCCCGG (SEQ ID NO. 249)

.....Rv234T7.seq:.....
TGACAACGCGGCGGCGATTACCCCGCTACCGCAGCAGCATGACGCGGTAGCGAACACCGCCGGATGCAGCGCAGGTGC
GTCGATGTGCTCACGGAATCGCCCCGGCACCGCATCTCGAGGATCACCAAGTCCACCCCTGCAGCGCGACACCGAC
GATTCCGTACACCGCCACGCCGATCAGGCCCTGGGCCAGCTGATTGGAGCTGGCGTATATGGCGGCGATGGTGACGAT
GGTCATCGCCTCTTACATTGTGGCGGCCAGAACCCAGGCGTTGGGGCGCGGTCGATGAACACTAGGCGACCANATCC
CCGGGGTCAACAGGTTGACCATCC (SEQ ID NO. 250)

Clone Rv235

.....Rv235SP6.seq:.....
CGCGGACATCCCGAACGAGGACACGCGACCGCTTCGGTGTGTGATCTATCAGGGCTCGCACCACGCGCAACCGCTTCC
GGCTACCTAGACGCGGT (SEQ ID NO. 251)

.....Rv235T7.seq:.....
GCATGCGGGTGATGCCGTTCTCAGTGCAGAACAGCGTTTCGACGCGGCATACCCAGCCGCACATGCCGTGCACGCCGNN
GCCGGGGCGGGAATCT (SEQ ID NO. 252)

Clone Rv237

.....Rv237SP6.seq:.....
CTCAAGCTTCAGNCCNTCTAAGCGGTCTGCGCGGCGATCGCAAAGATCGCCCTTTGCCGGCGTTGGGGGCTTCTGCTC
GGGGGTGTTGTACACCTTCTCGAACACCTCGGCACCGACACCACCACCGTCGGCTTGAACACCGCCAACATCGGCAGC

ANATCTTGATGTCCTGGTGAATCCACGGTGACTTTGGAGTGGAAGGCGGCCATACTGATCGCGCGCGCCACCACATGA
GCTAGCGGCAGGAAAACCAGCAGCCGCTCACCCTTGCGCAGCAGCGTCGGGTGATATGCCTGGCGCCC

(SEQ ID NO. 253)

.....Rv237T7.seq:.....

AGTCGAANGTCAGTCCGGTCTCCTCTCCGACTACGGCCAAGAACTGGGGCGACGGTGTCAGTGCAGAACAGCGGAAAC
TGGTGGCGCCCTAGGCGAGCGAACGCTCACAACGGCGGTGACCGCTTCTGGTCGTGCACCATCGAGCCGTGCCCAGC
CCGGCCGCGTGCCGTGAGCCGCATCCACTGGATGCCCTTCTCGGCGGTTTCAATCANGTACAGGCGACGTTCCGCCACC
ATCGTGCCGGGCGACGGTTAGCGAGAAACGCCGACTTCACCGATTGCCTCGGTGATGxxxxx

(SEQ ID NO. 254)

Clone Rv23

.....Rv23T7.seq:.....

AGCTTCGCGGCGTGCGGATCGCGGTTCAAGGCGCGCTCTTCGAGCACAACGAGCGAAGACAGCTCGGCGACGGAGCCT
TTATCGACATCCGTTTCGGGCTGGCTGACCGGCGGCGAAGAACTGCTGGACGCGTTGTTGTGACGGTGCCGTGGCGAG
CCGAGCGCCGTGAGATGTNCGACCGGGTGGTCGATGTGCCGCGGCTGGTGAGTTTTCACGACCTGACCATCGAAGATC
CGCCGCATCCGCGAGCTGGCGCGGATGCGCCGGCGGCTCAACGACATCTACGGCGGCGAACTGGGTGAGCCCTTCACCA
CCGCCGGGCTGTGCTACTACCGCGACGGCTCTGACAGCGTCGCCTGGCATGGCGACACCATTGGTCGCGGCAGCACTG
AGGACACTATGGTGCGATCGTCAGCCTCGGCGCCACCCGCGTCTTCGCGCTGCGGCGCGCTGG

(SEQ ID NO. 255)

Clone Rv240

.....Rv240SP6.seq:.....

AGCTTCAGCTGATACTCGACCAGCCCCACTCGGGCCAATACGTGAATGTCTAGCATCTTCACCCGTTACGGGCTANT
CGAGTAGTAGACATTGATTAGCCTGAACGTACCTCCGACGCCAGCTGACGAACGGGTATGACGGATGGATTTCGTGGT
GTCGCGCCCGAGGTCAATTCTGTTACGGATGTATCTCGGGGCCGATCGGGCCGATGTTGGCGGCCGCGGCGGCCTGG
GACGGACTATCCGACGAACCTGGCGGTGGCGGCTCTGTTGGGTTCGGTACCTCGGGCCTGGCGGATGCGGCGTGG
CGCGGCCCGCGCGGTTGCGATGGCNCGCGCGGT

(SEQ ID NO. 256)

.....Rv240T7.seq:.....

CTGGTCATGGACGTTGCTCCGGTAGTGGCTCACTGCCGATCCTCCTCGTTGAGAGTGCCACCTCAGGGTTGGGTAGGG
TTGGGTACTCGAAACCAAGTTACCCACCAGTAACACCGTCAAAATATATCCGTTGCATAGGTCAATGCAAGTTGATGT
GAGCTAGATTGCACCAACTAATAACCAACCGGTTGGGTTAGCGGTGATCCTGGCCGTGTGGTCTCTCACCTGCGG
TGATAGCGATCAATGAAGAATATCGGAGTTAGGGCGGCGAGCGCTGGCANCCTAGATCATCGGCTCACGCGGATG
CGGCCTCTTGGTACGGACATGCGCGCG

(SEQ ID NO. 257)

Clone Rv241

.....Rv241SP6.seq:.....

CTCGTGAGTAGCACCCCTGTAATTTGGGATCGGCAAAAAGGCGAATCACCGCGTGCCACGACACGCCGGGAGGGACN
ATCTCGGGCGGCTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGTCTGCCCTCCGACCGCG
AACATTCGGGGATGGCAGCAACCTGG

(SEQ ID NO. 258)

.....Rv241T7.seq:.....

GGATCAACTACCGGCCAACGGTGATTCTTGGGCGCGCTGACGCGCGAACGACCCAGCGACACATTACGAGATGGCC
AGCGCGTGCCGGGCCACGATGTTGGTGCTCGGCGGCTACTCCCATGGTGCGGCNCGTGATCGACATCGTCACCGCCGC
ACCACTGCCGCGCTCGGGTTCACGCAGCCGTTGCCGCCCGCAGCGGACGATCACATC

(SEQ ID NO. 259)

Clone Rv243

.....Rv243SP6.seq:.....

AGGACCGTCAGCACGGCGACGTGCTACTCGCCGAGCAGTGGGAATCGCTCTGCAGCAAACCATTACTCTGCGCGACGT
TCGAGATGACCTTCTGAATGGACGGATCTACCTGCCGCGCGACGACCTGGACCGCGTATGCGTCCGCCTCCGCCTGGA
CGACACCGGGGCACTCTATGACCCCGACGGACGGCTCGCGGTACTGCTGCGGTTACACCGCCGACGCCCGCACGGTACG
CGTCGGGACTGCGCTGAGTCCANCCTCGACGCCGTAGCGCTGCTGCTGTGCGGCCATGTCTGGCATCTACCGCCGTCG
CTCCCTTGA

(SEQ ID NO. 260)

.....Rv243T7.seq:.....

CGACTCTGTTGGCCACTGCGGGTCGATCTTGCGGCGCGCCCGGTGCTGGAACGCCAGGTACACCGCGCGCGCACCGC
GGTCAGCGCGTCGTTGGCCAGCGTGGTCACATGGAAGTGGTCGACGACGAGCTTGGCGTTGGGCAGCAGCCCGGGCGT
GCGGATCGCCGAGGCGTATGCAGCGGCGGGGTGATGGCCACCGTACTGGATGCTCTCCCGGAAGTGGGTGTGCGCG
CTTGACGCCATGCCAGCACCGCGCGCGCGCGGCTTCATGCTGCCATAAACCTGATACCGGCCAGGTGACNA
ACCNGTATCCACGGTCAACCC

(SEQ ID NO. 261)

Clone Rv244

.....Rv244SP6.seq:.....
CACACGGACGGCGGTGCGGACGCAGCTGACGCGCATGGTGGTCAGCATCGCGGCGGGTCTGCTGTTGTATGCCTACTT
CGCGCCGCGCAAATGCTGGTGGGCGGCGGTGGTGGCGCTCGCATGGCTGGGCTGGGTGCTGACCCAACCTCTCGAACCA
CACCGGTGGGTGGGCTGGGCTATGGCCTGCCATATCGGCCTGGTGTCTACN (SEQ ID NO. 262)

.....Rv244T7.seq:.....
CCGATATCCGAGCCGATAGCTGGCGGGCTCGGGTGGTNGCCAGCGGCGCTGCGACGAAAGTGTGACCGTCATGAAACA
GACACCACCGGCGGCCGTCGGCCGTCGTCACTGCTCGAGATCTCAGCATCCGCAGCCGGTGTGATCGCGCTTTCGGC
GTGTAGTGGGTGCGCGCCCGAGCCCGGCAAACGCCGGCCGACACAACCCCGGAACAGGAAGTCCGGTCACCGCGCC
(SEQ ID NO. 263)

Clone Rv245

.....Rv245SP6.seq:.....
GCTTCAGGACAAATTGNATCCCTATGCACCCGTTGTACGCCGATGAGTGAAGACTGCACGCAATCGCCGGAATCCGG
CAAAACCCTGCACAAGCGAAATCAACCGGAGGCTGACAAGGCAACGTCGGTGATCCGTACCGCCTGGTTGGACAAACG
GCAGAAGGGCGCTCGTCCGGTCCATCTACGCCGAGCACACTGGTGATAGCGCCATCGGCATCGGTGCGGCCACGGTGG
AGACGAACGTCGCGNCGGCTCTGGGTGAGTAACCGCCGACCAGTTCTCGGGCAAGCTGGTCAACATCGGGCGCCACG
TCTCCAAC (SEQ ID NO. 264)

.....Rv245T7.seq:.....
GTTTGGCGGCCTTATTGCACTGAGGTGCTCAATTGACCCACAGCGGAAATGCCGACTATTGCGAGGCCTCCTTCGCCT
TGGCTGCCGAGATGGGCTCCGCGGGAACCGCATGCAGGTATATGACCTCGGTTTCTCGGGTGCTACCGCGTGCCCTTG
TCGAGGATGAACTCGGCGTTGGAATTGTCCAGCCGGCCCAATTCATCGAGCGCAGATTCTGACACATGGCCGGCGGCG
ACATACCTTCACCGTGGATCTGCTCCACACGGACCGCCTGTGCGGATCTGCTACGGGTAAAGGAATTA
(SEQ ID NO. 265)

Clone Rv246

.....Rv246SP6.seq:.....
GCGCACTCCTCCTTATCGCTCCGCTCTGCATCGTCGCGGCGCGGTGAGGTGCAAACGCCTTCGGGGGTGGGGGTCTTG
CGGAGCACACCGGATACGGAGCGCAACGCGTCGCGTTGTGCGGGCAAACAAGTGTGCAAGNNCCAATGCCATGTCCAG
CAGCTTATCAGTGTGCAACGTGCGAACGTGCGGCCTTCGCCGTGCTGAATCTCTACAAG (SEQ ID NO. 266)

.....Rv246T7.seq:.....
CGGTGAAAGCCACCATTCGCGGGTGGGGCGCGGGCTCGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCG
CGACACCACCGGCTGCGCTACGTGAGCCATACCGGGCGGAGCTACATCGGCTCGGCCGCTAGTGTTGGGNCCTC
TTTCGAGGTGCGAGGTGCA (SEQ ID NO. 267)

Clone Rv247

.....Rv247SP6.seq:.....
TGTAATTTGGGATGGGCAAAAAGCAAANCAACGCGTGGCCACAAACGCGGGGAGGGACAATCTCGGGCGGCTAGGGCT
TCTCGCGGGAAGCCCGAAACGTACGGCGTTTCAACACGTGCGCTGCGCTCCGACGCGAAATTCGGG
(SEQ ID NO. 268)

.....Rv247T7.seq:.....
CTTGGGCAACATGCTGAGGATCGCCTTTTACCACGCGGTGCGGGTGGCGTTGCATTAGCTACCGATGGTGCGCTTG
TTGCAGGCCCGCGGATACCGAGTGCCGGTAACCATCTTGTGCTGCAGTTTGTCCGCTGATGGCGACCTTGTGCG
GTTGATCACGATGACGAAGTACCGCCATCGACATTGGGGCGAACTCGGCTTGTGCTT (SEQ ID NO. 269)

Clone Rv249

.....Rv249SP6.seq:.....
GCATGCTTCATTATCTAATCTCCAGCCGTGGTTTAAATCAGACGATCGAAAATTCATGCAGACGGTCCCAAATAGAAAG
ACATTCTCCAGGCACCAAGTTGAAGAGTTGATCAATGGTCTGTTCAAAAACAAGTTCTCATCCGGATTGAACCTTACC
AACTTCATCCGTTTCATGTACAACATTTTGAANCATGCTTC (SEQ ID NO. 270)

Clone Rv24

.....Rv24SP6.seq:.....
ATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTGGGGCGCCGGGCCCCGG
GCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCCACACCACCGGCTGCGCTACGTCTATCCATAACCGGCC
GAGCTACATCGGCTCGGCCGCCATTGTTNCGCCCTCTTTCGAGGTGAGGTCTATACCGATTGCGCATCCG
(SEQ ID NO. 271)

.....Rv24T7.seq:.....
TCCGTACTGGTCGGGTACGCTTCGGTCGCACTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATA
GCCCCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGTAGAAGGTGCGCGAGCGCTCGGCATTGGTCATCGGGATA
TGCCGCTCGGGACGGTCAGAACCTCGGGTCCG (SEQ ID NO. 272)

Clone Rv251

.....Rv251SP6.seq:.....
GTTCTCGCACGATTTCCGATTAGCGGGATGGTCTCAATTGGGTATGCGGGGAAGGCGCTGACATTCGCCGCGATTAGC
TGTTTGATGGACCGGGGTGATTTTGTATCACGGAAATGGGTGTTTATNCAGGTCGCACGCTTTCATCCGGGGCGGAA
CG (SEQ ID NO. 273)

.....Rv251T7.seq:.....
GGGTGTGCCTGCTGTGTATGCACGGCATAACGACATCCTTCCCCTGAAGACCCGCGGTGGAACAGCCACGTGTCCATC
ATCANGGGGTCAACCCCGCCAAGGGCGACGGCAGCCAAAGTTGCGCCGACCGTTAACCTAGTGCTGTTAGCTTCATT
GCTGCGAGCAAAACAGCTGGTCGGNCGTTAGGAATGAATTGAACTCAACCGATTGGTGCCGCCGTAGGTGTCCTGG
CTG (SEQ ID NO. 274)

Clone Rv252

.....Rv252T7.seq:.....
ACTACCCGGCCAACGGTGATNTCTTGGCCGCGCTGACNGCGGAACGACGCCAGCGACCACATTGAGCAGATGGCCA
GCGCGTGCCGGGGCCACGANTTGGTGCTCGGCGGCTACTCCCANGGTGCGGNCGTGATCGACATCNCACCGCCGCAC
CACTGCCCGGCTCGGGTTCACAGCCGTTGCCGCCGCGACGGACGATCACATCGCTTTTATTTNNTNTTCNGGAAT
CCCTCGGGCCGCGCTGGCGGGCTGATGA (SEQ ID NO. 275)

Clone Rv253

.....Rv253SP6.seq:.....
ACGTCGGGANACTGTTTCGCTTCATCCTCGTCTCGGCGGATTGGTCTGCTGCGCCGACCGACCGATCTTCAGCGGGG
GGTCACGCTCCGTGGGGTGCCGTTACTTCCGATCGCCAGTGTCGCGGTGCTGTGGCTGATGCTGAACCTCACCAGCT
TGANTTGGATCGGTTCCGGATCTGGCTGGTGCCGGAACGCNATTTATGTCGCTACGGGCGCCGGC
(SEQ ID NO. 276)
.....Rv253T7.seq:.....
GCTCAAAGGCACTACTGGCACCAAGGCCACACGTACCTGTGACTCCTGCGCCGACCCGCGGAGGTCTGGCCGTTA
CACCGAACGGGAGCCGGGAGTTGGTACCATCGAACAAGACAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTCG
ATGACGGGTC (SEQ ID NO. 277)

Clone Rv254

.....Rv254SP6.seq:.....
CGATACCGGCTGCTTACCAGACATCCACCATGCCACCCGAATCACCAGCAGCGCCGAAATCGCACAAACAGCTTGACG
CCTTGACAGTTCCGCGATTGGAATTGCCGACGGTCTCTGACGGCGTCGACCTTGGCAGCCTCTACGAGCTCTCGGAAT
CACTTGCCAGCAGGGGGTTCGATGAGTGTCACACCGAAGACCTCGATATGGGCGCAATCCTGGCCGACACATCCAAC
CGGGTGGTTGTGTGCTGCGCGCCGGTGGGGTCNGCAANACACTACCGCGCCGCGCTGGCGTTGCGCGCGGCCGAAT
ATGGCCGCACTGTGGTCG (SEQ ID NO. 278)

.....Rv254T7.seq:.....
CGTCGTCGTCGTTGATGCGATAGCCATCCCGTCGGGCTACTCGCCATCACCAGTACGCTTCGCCCCGAAGCCGCGC
GGCGATTTCCGCTGCGACCAAACTGACCGGGGCCAAACCGGTATTGCTTACCGGCGACAACCGGGCCACCGCCGATCG
GCTCGGTGTACANGTTGGCATCGACGACGTACGGGCGGGCTACTGCCGACGACAANGTCGAGCCGTGCNGCNGCTG
CAAGCTGGAGGTGCCAGATTGACCGTGGTGGTGACGGTATCAACGACCTCCGGCCTTAGCGGCCGCGCATGTCGCAT
CGCCATGGGACAGCGCCGAC (SEQ ID NO. 279)

Clone Rv255

.....Rv255SP6.seq:.....
GCACGCAATCGAAGTCACCCAAACCGGGCGGGCCAGGCGTCTNACGCCACGTCTNACCAGCCGCAACCTCAACCCGGCC
ACGGCGAGCTCCTGATCAAGGCCGAGGCCATCGGTGTCTACTTCATCGACACCTACTTCGCTCCGGGCAATATCCGC
GCGAACTCCCGTTCTGTCATCTGCTCCGAAGTATGCGGCACGGTGGAAGCCGTCGGCCAGGGGTTAC

(SEQ ID NO. 280)

.....Rv257SP6.seq:.....
GAACCTGACACCCTGGTGACGGGTGAGCACGGACTTGATTTCTTCNCATTGCTGGCGCTGTTGAGCACACCACGCC
GCTGACGGCCGTCGCGTCTCTCGTGTGCTCGGTTGGTGAGCGCGCTGCCCGCGGCCNAACATCNATAATCAAGCGT
ATTCGTCAACAGATATCATCAATGTGCGCGCTGGACTATTCAAATCATCGATATACTGGTGACCTGGTCTCTCGCCAT
CGATCAATGGCGATAGTCACGCAAATCGTCACGCGATCGTCGGCGTCCAGCTGGCCGCTGCCAACAGATGCTGCAA
CCATCGGGGTGGTATCACCGCGGTGCTCGGCGATGGTCCACAATTCTTGGCGTCCAAGCCNAAACATCCCGGGCAT
GAATTCACCGGCATGCGCN (SEQ ID NO. 282)

.....Rv257T7.seq:.....
CTATCGTACCCGCGCCGGTCACCTTCTGGATATCGCCGGCCTGGTCAAGGGGGCGTCCGAGGGAGCCGGGCTGGGTNA
CAAGTTCCTGGCTCATATCCGCGAATGCGACGCCATTTGTGAGGTGGTGCGGGTGTTTCGTGACGACGACGTGACTCA
TGTCACCGGACGGGTCGATCCCCAGTCCGACATTGAGGTGCGTCGAGACCGAGCTGATCCTGGCAGATCTGCAAACCT
GGAGCGGGCCACGGGCGGGCTGGAGAATGAAGCGCGCACCAACAAGGCGCGCAAGCCGGTCTACGAAGCGGCACTGCG
TGCCAGCANGTGCTCGACGCGGGCAAGACGCTGTTGCGCGCGGGGTGGATGCCGCCGCGTTGCGCGACTGAAACT
GCTGACCACCAAGCCCTTCTGT (SEQ ID NO. 283)

.....Rv258SP6.seq:.....
TACTCAAGCTTCAGGCCGCCACGTCCGCCGTCCGTGGCGACGTGACCTCGAGCGCCGAGTTGCACTCGACATCGCCG
CCGGCGCATGCCGACATGAACCGGGCACTCACCGCAAGCCCGTCGGACGTCAGGTCGATCGACTCCGTTCAAGCACC
GGATCGTCCGGGCAACTCGCGGCCTCGGCCTGTGCGAACGGCACACCCGTCGTGGCGGCNCCCGCGCGGAAGTGGGC
TCATCACGGTCGTTGCGAGCCGGTCGCGTCAACCGGTACCGACGCCGTC (SPD ID NO. 284)

:::::::::::Rv258T7.seq:::::::::::::
 CCGACATCGAGTGGGCTCGCAGTGACTTGGCGACCTCCAAGCCACCGGTACCCGCCGCGCGGAAGCCAAGGACGACG
 ACGGCCCTTGCCGGATAGCTGCGCCAGGCGTTGCGCCAACTGGCGTCCAGCGTCGCCACGATCGTCAAAGAGCTTCATC
 TGCCGAGTGTGTGCGCCATCTCATGGCTCCAAATATGGAATTAGGTCCCTGGGCCGACTGACGACAGTCCCTCAGCGAC
 CGGATTGCGCATCCCGCCTTGTACGCTACTCCGCAAATCCCGGGCTTGCCTCCGCGGAAGCGAACTCGGCGGGCGCTAC
 GTGGTGGTTCACTTCGGCCGTGCGCACTCGGATCGACGGGCCGATGGTGGCCGGGCCCGCGCGTTCTTGGTCATCCG
 ATTGAGT (SEQ ID NO. 285)

:::::::::::Rv259SP6.seq:::::::::::::
 ATACTCAAGCTTGTCGCGGTAAACCGCACGCAGGGCGGTGGGTGCGGTGTCAAAGACACCCACACTTCTTTGCGGTTCC
 GGTGATCTCGACACCGGCGCGGACGCCAGCCACCATATCGCGCGTAGATCGGCGCATCAGCGCGTCCGGCTATCGCCTGGGT
 CGCGCCCAACCGGAATCGGCCAGCCGACCGCAATGGGCCAGCGTTGCCAGCATCAGTCCGGCGCGGGCCGACACCAAGTGA
 CGGCAACGGTGAAATCGCGTGGGCGGCAACGCCGGTGAACAACGCGCGGGGCATCCTCGCCCGCCAACGACCGCCAGGC
 AGGGTGCCTGGGCCATCATCCGCAGCCGA (SEQ ID NO. 286)

.....Rv259T7.seq:.....
TGGACTCATAACGATCGGGTCAGCGACGCGCAACACGAACGGCCGGACGAGTGGGCCAGGGTCGCGCCTCCCCTACA
AACAGGATCCGTTGCCCTGCGAGCGACAGGCTCCGGTGC GGCGTTGGGCGCCGTGCTCGTCCCAGCGTCCGGTCCCGG
TCGCGCGGCGACGCTTGTTCCTCCATACTCGCCCTAATCTCGAGCGACCGGTACCCGACGGCAACCTCCCAAAA
TGCAATCCCCCAAATGCAATGCGCTCGAGCTATTTCTCACACGACCGCTAGTTGCGGATCAGAAATCCGTTGGGCGC
GGAAGTCCAGCCGAATTTGTTCTCCGCTCCGCATCATGCTTGAATCGTTTGAAATCATCTCATATGCCTCGATC
GCTTCATAGGTCAAGCCCAAACCCGGCAGGATGGGTGGCC (SEQ ID NO. 287)

.....Rv25SP6.seq:.....
CTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATG
ACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTAGTGGTTGCGCACGTAATTCGTCAAGGT
GACCGATCCCCTGCTGTCTCACTCGCCTCACAGCGACCACCACGGCTGGCGCTCAAGGCGGGCACGTGCGGAGCAGAT

GAGGAATGTGCGACGTCTTGATGCAGCCTGTGAGAACACCGAGACCCTCGACGAACCTTACGATCGAAACCGCTTAGGC
CAACCGGTGACGGGGGTGTCTTTCCGCGGCTAGGGCGCCTTATCGTCCGAAGGCCGTGGGTGGTGATCGCCTTCTGGG
TCGCGCTTGCGGGTCTGCTTGCGCCGACGGTGCCGTCCCTGGACCGATCTCCAGCGGCATCCAGTGGCGATTCTGCC
ATCGG (SEQ ID NO. 288)

.....Rv25T7.seq.....
CAGGCATGCAAGCTTGCGATGTATCAACACGCCGTGCGCAGCGTGAGCCGATAGTTGACATCCGGCTCGGTGAAGGT
GAAATCGATGGCCAGGTGAGGTCCCATGCGCGTGGGCCATTGATGCTGATCGCCAGGACGTCAAAGATTGGTCCGG
CGTCAGCTGGGCGAAAAACGTGGGCGCCGGGACTTGCCCGGAGCTGCCCGGGTTCCCGTCGCGCAGCTCGGCGGCC
GGTCAGAAAGAAATTGCGCCAGGTGCGCACTCCGCGCCGTAGGCCAGCTGCTCCACGGTGTGCGCATATAGCCCGCG
GGCGCAGCGTGTGCTGCTGCGGCAACACCGCATGGTCGAGAAGCGTTGCCGCCAACGGAAATCACTGCGTCAAAG
CTTCGCCGGGCCACTCCAGCACTCCGTC (SEQ ID NO. 289)

Clone Rv260

.....Rv260SP6.seq.....
ATACTCAAGCTTGACCGACGCTGATCGCACCGCACGCGGGAACCTCAAGGGCACTACTGGCACAAGGGCCACACGTC
AACCTGTAACTCCTGCGCCGACCCGCGCGAAGTCCTTGCGCTTAACACCGAACGGGCCAACCCGGGAATTGGGT
CCATCAAAACAAATAGCAGGTGCTGGGCGGAGTGTTT (SEQ ID NO. 290)

.....Rv260T7.seq.....
GTCGTCGTGTGCTGGGCGTCCGTATCAGCACGCCCCAGAAATGGGGCACAAGAAGGATTCTTGAACGGTGGCTGTG
CAAGATCACCTCGCCCAAACTGCTACGGGCACTTCTACATCGAGCACAACCGTGGCCATCACGTCCGCGGTGTCCA
CACCGGGAGG (SEQ ID NO. 291)

Clone Rv261

.....Rv261SP6w.seq.....
ATATGCTTGTGAGCTTTTCGGATCGCAGCGAGTCGTACCCGCGCCGGTCACCTTCGTGGATATCGCCGGCCTGGTC
AAGGGGGCGTCCGAGGGAGCCGGGCTGGGTAACAAGTTCCTGGCTCATATCCGCGAATGCGACGCCATTTGTGAGGTG
GTGCGGGTGTTCGTGACAAACGACGTGACTCATGTACCGGACGGGTGATCCCCAGTCCGACATTGAGGTGCTCGAG
ACCGAGCTGATCCTGGCAGATCTGCAAGCCCTGGAGCGGGCCACGGGGCGGCTNGAA (SEQ ID NO. 292)

.....Rv261T7.seq.....
GACACCTGGTCACGGGTGAGCAGGACTCGATTTCTTCGCTATTGGTCGGCGCTGTTGAGGCACAGCACGCCGCTGAG
GCCGTCGCGTCTCGCTGTGCTCGGTCTGGTGAGCGCGCTGCCCGCGGCCGAACATCGTAAATCAAGCGTATTCGTC
AACAGATATCATCAATGTGCGCGCTGGACTATTCAAATCATCGATATACTGGTGACCTGGTCTTTCGCCATCGATCAA
TGCGGATAGTCACGCAGATCGTCACGGACATCGTCTGCGTCCCAGCTGGCCCGTGCCAACAGATGCTGCAACCCATCG
GGGTGGTATCNCCGCGGTGCTCGGCGATGGTCCAACAATTCTTGGGTCCAAGCCCGAAACCATCCGGCCATGAGTTC
ACCGCATGGCGCAACGGCTGGTGCCGGGCAAAACGCGGCGCATCGAATTC (SEQ ID NO. 293)

Clone Rv262

.....Rv262SP6.seq.....
TGTAAGAGGTGGGTCCCGTCCAACCTCGCGGCGGCGCGCATATGCCTTGCTGGTCTTGCTCATTTGATATCCAATC
TATGGGTGCTGGTTACTCAACGGGCCGAAGCTGGCCCTCCACGGGTAGGGTCTATTTCGACGGTGATGTCC

(SEQ ID NO. 294)

.....Rv262T7.seq.....
CCCGAATCCGGTGGCCGGCAGGGGGCCTGGCGACGTGGACACCTTCTAACTTGTCTTTACCGGTCACTGTTGCACCCC
AACACCTTTAACGACGTGGACGGACGTTACATCGGATTCGACGGTGTATCCACAGCGTTGCCATTGGGCACACCCAC
TACGCCAATTTCTCCGACTGGGACACCTACCGCAGCCTCGCCCCACTGCAGGACTGTTGTTCCCGCAACGGGCCATC
GACATGATCCAGTCGTTGGTGACCGACGCGGAGCAGACTGGTGCGTATCCGCGTTGGGCGCTGGCGAAATTCGCCAC
CGGCATGAT (SEQ ID NO. 295)

Clone Rv263

.....Rv263SP6.seq.....
TTGAGATGCTGGTGGGATGCCGATGGTTGGAACATGGTCCCCTGGCGTCGAATACGCGCGAGCGCATGAGCTACCCG
GTTCCGAACAACGTATCGAAGAACTCGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTATCCCAACTC
TAACTGTGCTATCGGATCTGCGTGAATA (SEQ ID NO. 296)

.....Rv263T7.seq:.....
CGTAATCACGATCCCGCTGAGACACTTGACCTTACGGCCGAAGTGAAGTTCGCTGCTGCTATGCCGACACCCGATTTC
ATACGCTGCTGTACACGACGGCCGGGCGGTGGCTCCATCACGCTCAACCGCCCGGAACAGCTCAACACCATCGTCC
CGCCCATGCCGACGAGATCGAGGCCGCTATCGGGTTGGTGAACGCGACAGGACATCAAGGTATCNTNCTGCGCG
GTGGCGGGCGCGCCTTCTCCGGCGG (SEQ ID NO. 297)

Clone Rv264
.....Rv264SP6.seq:.....
CAAGCTTAAGCTGGTCCGGCCACTCCATGAGCCGTAGTGCAATGGTTCTGTCACGGCGAGGCCGAAGTTCGCATAAA
CATCCCTGACGAAAGTCTCCGGCAAGCCGATTGCTTCTTCGGGCGGCTTCTTGTGGATTGTCCGATAACCCGGTCCCT
CATGCTGGAAGTTGTGCGCACTCTTTCTCCGCGATGTGGGTAACGACTCGTCATTGAGCAAGAAGTACGTGCACA
GGCATCGTCCGCGGGGCTTCAGCACGCGGGAGATCTCGTCCAGATAGTGTCCACGTCCGGNGGGAACATGTGGGTG
AACACCGAGGTNAGAAACACNCATCCAACGACGCATCCGGGATATGAAAGCGAAA (SEQ ID NO. 298)

.....Rv264T7.seq:.....
TATGGTCTTCGTCGACCACTAGCTCGTAGGCGCCATGAGCCAGCGACTGAAGCCGCGCCATGCCTGCACGGCCCGCTC
ATCCAGCGAGGCGCCATCTCCCGCAGATAGCCTGCCGCTCGGCGCGCACGCTGTCCGGATCGCGTCCGAGCTCGTC
GCTCAGCGCAGCGACGCGCTCGTCATACCATCGGGCATCCAGCAGTTGGGTAACCTCAACGGGGTCCGTTCGTAGCGG
CGTCATTGATTAGCAACAATACCGATGCGCTGCAGCAACTTTTCGAGTCCGATGCGGCCCCACCTCCCGTGCAGTCAC
TGGCTAGCCCCGTCATGCCGTTGTGTGATGGCACGGCAGCGGGCTCGTAAACCTGCGGTCTCAGCTCGCTGG
(SEQ ID NO. 299)

Clone Rv265
.....Rv265SP6.seq:.....
GCTTAGCGGTCTTGCTCGAACCGACATTGCGTGCCACTCATGAGCGGGTGGCGGTGCGGGTGCTTACACATCT
(SEQ ID NO. 300)
.....Rv265T7.seq:.....
GTATCTGGCGCCTCTCGAATATCCTTGAACGTCCGCGGTGCCACCCAGATAGATCGCAGCGCCCTGCAATGGAGTTC
CCTTTATGGCCTCTCTAGCCTCCCGCTTGATCGGCTCGACCCGAGAGATGCCCTCGGGCGTTGCGGGATCTCCCTCCA
(SEQ ID NO. 301)

Clone Rv266
.....Rv266SP6.seq:.....
CTTCACGCCGATCCGCGACCGGAACGCGACGGTGACGGTGGGCGACAAGGTTGCGTTGGTTCGCCGCGGCGCTGGGCG
ATATCAGCTCACCCGGTTTCGAGGTGTTCCGGCAGCGGACGGTGCTGCAGACATTCTTGAGCGTCTCGACCGGCCCCG
ATTCGGCCTTCAACATCGTGACGCCGATTTTCGGCGGTACCGCTCGGGCGCCGAGTCAAGGCGGCGCTGAGCTAAAGCC
GGGCATTGCGCGAGTGGTAAACAAGTTCCGGTGACTTCGGTTGACCGACTCGACGGGCTCGATCTGGGCGCGCTGGACC
GGTATCTGCGTTTCGCTGGGGATCGGGCCNACCGCNANTTGCCTGCGANCTGATTCGGGTGGAGCTCCAATCTGACTT
CCGG (SEQ ID NO. 302)

.....Rv266T7.seq:.....
GCAGCTACCGACCCTAGCGACGAGTGTGTTGCGAGCGTCGAATGTGAACGTTTCGGCGTGATTTCGGCGCGCGGGTTCCC
GCTCTCAGCGCACGTTTCGGCGCCGAGNGGCTAGTCCCTGGTTAAGCAATGTCTCGGTGCGCCGACGACGCGCATG
TCGCCAACCCGTCNACCGCGTTGCGCATGTCCGGTACCGACGGAAACGACGGCGCGATCCGGATGTTCTTGTCTCGG
GATCCTTTTCGATACGGGAACGACCCCCCGCCTCGGTACCGCGATACCAACGTCCTTAGCCAANGCTACNGTCCGGCG
CGCGGTCCCGGGCAACACGTCGAAGCTGATGAANTAACCACCTTGGGCTCGGTCCAAGANGCGATCTTGGACTCCTT
AACCGCTGATNCAA (SEQ ID NO. 303)

Clone Rv267
.....Rv267IS1081N60.seq:.....
TCCCCATCGGCGCCGGACCGTTTGAAAGTCCAAGCACGGGTGGGATGGAATCGACGACAGTTGAGCGCCGTCCGTGGC
CGTGGTCAGCAGCTGTTTCGGAACGCACAGGTACATCCCTTCGACATCTCACCGACGTGGCACGGGCGACATCAAC
AGGAAGATTGACGAATCCCTCGCAGGCGCGGACGTCGCGAGGCCAACGCCAACTACGGGGCCACGAGCATCTCCG
CTCACGACCAAGCCAGGCTCANCCACCAAGTCGGCCGCGCTCTCCCTCGCCCCCTGGTCTCCGGGGCCCTT
GTTAAACAACCTACCGGAAGTCCACCAATCCTCGCTGCATCTCGACACCGTCCGCTCACTCCCTTCTCCGCCCCCTC
TCCACACNACACCTCTTGATTAAGGTACGGAGCGGTCACTTTTCGTGCGACGAAATTCGCAATCCGGCCGCTCG
CGCCAGAGAT (SEQ ID NO. 304)

.....Rv267SP6.seq:.....

CGGAAAGTGGATACTCCCAGCAGGTAGCAGGTGCGCCACCACGCTGGTCACTGCGCGTTTCACTCGCTTGGCGCGCTGC
AGCAGCCAGTCCGGGAAATAGCTGCCCTGGCGCAGCTTGGGGATCGCGACGTCGATGGTTGCGGCACGGGTGTGCGAA
ATCACGGTGGCGGTAGCCGTTGCGCTGATTGGACCGCTCATCGCTGCGTTGCGGGTAGCCCCGCCCGCACAGGGCGTC
GGCTTCAGCCCCCATCAAGGCGGCGA (SEQ ID NO. 305)

.....Rv267T7.seq:.....
GGCCGAGTCCAGCACTTCGCACTATGTGCAGACCAANACCCGGTGGTTCGCCGCGCTGCGGCAGCGGCTGGCAACGGC
GCCGGTGATCACCGAGTGGTGCNAGTTGCCGACCGGCACTTCGCCGCGGGCTTACTACGAGAAGGGCTGCGCGACG
TCATCAGGTATCACGTGTCGATGACGTGAGCGTTAACTTCCCCGACCAGACGGCGACCTCGCCGATGGACCCCGCT
TGTACCTGGTGTGGGCGCAAGCTAACGCCCGCCGANGCTATCGGTACTCGGTGGAAGCGCAGCCGGGGTTCGAAGCGC
TAGCGGGCAAGGTGCGGACGATCTCGGTACCTGGACCAACTACGGCGCTGCTGCCGCCACCGAATAGTNGTGGCCG
GCTACCGGCTGGTGGATTCCACGGGACATGTGGTTGCGACCTGCCGGCAGCGGTGGAATGAAGANGCTGGTCT
(SEQ ID NO. 306)

Clone Rv268

.....Rv268SP6.seq:.....
AGCTTCAAGGACATCGTCATCGCGACCAAAACCGCGAGCTAGGTCCGCATCCGGGAAGCATCGCGACACCGTGGCGCC
GAGCGCCGCTGCCGGCAGGCCGATTAGCGGGCAGATTAGCCCCCGCGGCTCCCGGCTCCGATTACGGCGCCCCGAA
TGGCGTCACCGGTGGTAACACGCTTGC CGCCTGGGCGGCGGCTGCCGGATCAGGTGGTATATGCCGACAAAGCC
TGCGTGATCGGTATCACCAACGGTGACAGCAGCCGGTTGTGCACCATCGCNAACGCCACCCCGGTCTCCGGGTCTGT
CAN (SEQ ID NO. 307)

.....Rv268T7.seq:.....
GCTCGCGGTCCAGCAGCAGACGTGTCTGACCCCGACGCCCGGCCCGGTTACCGAAACCGGATCGGCCCGCCGATGGC
CGCGGCCACGGCTCTGCCTTACCCGGCCCGGATACCAGCAGCCACACCTCGCGGGAACGCTGAATCGCCGGCAGGGT
CAAGGTGATTTCGGCGTGGCGGCGGTTTCGCGAATCGTCCACCGCCACCACCATGCGGGTGTCTCGAAGACGCGGGGC
TGTGCGGGAACAGCGAGTTAATGTGGCCCTCGGGCCCCATGCCAGCAGGTGGACGTCGAAATTCGGCCCGGGTCACC
TGTTGCGGCACTGGCGGCC (SEQ ID NO. 308)

Clone Rv269

.....Rv269SP6.seq:.....
AGCTTGTGATCGTCCGGCAGCGTCCGGCGAGTCAAGTCGAAGCCAGTCCGGTCTCCTCTCCGACTACGGCCAAGAAC
TGGGCGACGGTGTGATGCATACCAGCGGANACTGGTGGCGCCCTAGGCGAGCGACCGCCTCACAAACGGCGGTGACC
GCGTTCTGGTGTGACCATCGAGCCGTGCCATCCGGCCGCGTCCGTCAGCCGCATCCACTGGATGCCCTTCTCG
GCGGTTTCAATCAGGTACAGGCGACGTTGCCANCATCGTGCCGGGGCANGG (SEQ ID NO. 309)

.....Rv269T7.seq:.....
TTGGTGATCATCGNCCCAACGACCCGAGGCGATGTTCTTGCAACCGAGGAGTGTGCAAGCTGGGGCTGGCCTTCG
CCGCCGATCCGTCTCAGCAGCTGGCGAAGCTGTGCGGGTGAGGAAATTTCGAGGCTCGTCAACGGTGTCTTACTTG
TTCACCAACGACTACTAATGGGATCTGCTGTGTCCAAGACCGGCTGGTCAGANGCCGATGTGATGGCGCAGATCGAC
CTGCGGGTGACCACATTGGGTCTAAGGGTGTGATTGGTAGAACCTGACGCACCACCATCCACGTCGGCGTTGGTC
CCCGAAACAGCCAGACCGA (SEQ ID NO. 310)

Clone Rv26

.....Rv26SP6.seq:.....
GGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAGCT
ATTTAGGTGACACTATAGAATACTCAAGCTTGATTTGATCATCATGATCATCACCCGAAGTGTGGTAGCCGACG
TGTTTATCGTGGGTACCGTCTGCTTTCCATGGCGCCCTCTTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGG
GTATCGAGTTGTACTGGATGGTGTGGCGATGTCGGTGATCCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGC
TGATTTCCCGGTTGAAAGAGGAAATTGGGGCCGATTGAACACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAG
TGTTGACGGCTGCCGGCATGGTGTTCGCCGTTACCATGTCTGTTGTTGTGTTTTCAGCGATTTCGGAATT
(SEQ ID NO. 311)

.....Rv26T7.seq:.....
CAGGCATGCAAGCTTGGCGTGCCGTTCCAACCCGAATTTGGCTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTC
AACGACGACGTCTCCGCGGACACACCTCGATGCTGCCGCCATGGACGCGGTGGAACGCAAGCAGCTGATCGAGCTA
CAACGCCGCGCGGAACGCTTCCGCCCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTATGAC
GGCATGCCACCGGAGCGACGGCCAAGGCGGCGTGCCAGGTGTCGCCGGGCGCAGG (SEQ ID NO. 312)

Clone Rv270

:::Rv270SP6.seq:::

GGCATCTTGGCCGCCATGTTAGCCACACTGCCACCGGCTATAGAAGCGATGCCGACCGTCTGCCAGCACATTGCGGC
GCTCCTCCCTGGAAAGCAAGATAACCAAGCTCATGCCGTGGTTGTGGGTGGCGTGGTTTGGTTGGGTAACCTTGG

(SEQ ID NO. 313)

:::Rv270T7.seq:::

TCGGCTAATAATCGTCGACGCCGGCTCCTCTGCAATCGCCTTGGCGGTGCGCGGGTTGTCACCGGTGATCATCACGG
TGCGGATGCTCATTCGGCGCATTTTCGTGCAATCGTTCCCGTATGCCACCTTGACGATGTCCTTCAGATGGACGACGC
CGATGGCCCCGCGCTGCTGTTATCGGTCCATTCCGCAACGACTAGGGGTGTCCCCGCGGAGCTGATGCCGTGAC
AATGGCACCCACCTCCTCGGTGGGTGGGCACCGTGATCGCGAACCACCTTCATCACCGCAGCCGCGGCACCTTGGC
ATTCGACGGATG (SEQ ID NO. 314)

Clone Rv271

:::Rv271SP6.seq:::

CTCAAGCTTGGAGGCGTGGCGATCGCGGTCCAAGGCGCGCTCTCCGAGCACAACGAGCGAAGACNGCTCGGCGACGGA
GCCTTTATCGACNTCCGTTCCGGCTGGCTGACGGCGGCNAAATAATGCTGGACTCGTTGTTGTCGACGGTGCCGTGGC
GAGCCGAGCGCCGTGAGATGTACGACCGGGTGGTCTATGTGCCGCGGTTGGTGAGTTTCCACGACCTGACCATCGAAG
ATCCGCGCATCCGCTGCTGGCGCGGATGCGCCGGTGGCTCAACTAATTCTACGGCGGCGAAGTGGGTNATCCCTTCN
CCACCGTCGG (SEQ ID NO. 315)

:::Rv271T7.seq:::

CCTAGGTCAACCGTACCGTCATCGGATCGGGGTGACCGCACAGATGGACTGGAGCTTCGGCGAGGTGATCGCCTATG
CCTCGCGGGGGGTGACGCTGACCCCGGGTGACGTGTTCCGGCTCGGGCACGGTGCCACCTGCACGCTCGTCGAAGCAC
CTCAGGCCACCGGAAATCATTCCCGGGTGGCTGCACGACTGCGACGTGGTCACCCTCCAGGTGCAAGGGCTGGGCGA
GACGATGCAGACCGTCCGGACGAGCGGCACTCCTTTTCCGTTGGCTCTTCGGCCGAATCCGGACGCCGAACCCGACCG
GCGCGGGGTCAACCCGGCACCGACGCGGGTGCCGTTTACCCGCGGGGTGCACAAATCCCGACGGGTATGGGCTTGAC
CTGCCGACGGGGG (SEQ ID NO. 316)

Clone Rv272

:::Rv272SP6.seq:::

AGCTTGGCGTGACACCAACACAGGGCACTTAAGATGGCAATGCCCGCCTACCTGCACGTTTTTCGCGATGTCAGAGGA
TGCCGAGGGGAGAACAATGCGAGCACGGCCGCTGACGTTGCTCACCCTTTGGCGGCGGTGACATTGGTGGTGGTTGC
GGGCTGCGAGGCCCGAGTCTAGGCCGAAGCATATAGCGCGGCCGACCGCATTTTCGTCTCGACCGCAAGCGCGACCTCA
GCCGACGCCGGTGGAGCTACTGCTGCGGCCATCACGCCGCTAGGGCTCCGGCGGCGTCCGCGAACGTGCGGTTTG
CGAACTGCCTACCCGGGTCCGGCAGGCAACCGAT (SEQ ID NO. 317)

:::Rv272T7.seq:::

TCATGCCGTTGGACCGACCATCGGAGTTAGTTGCCGAACCGCGGGACCACCGCAAGCACCCGGTCTGGTCGCGCACC
GCGTCGGCCAACCGCTTGAGCACCAACACGCCGCGACCCCTCGCCGCGCACGAATCCATCCGCGTTGGCGTCGAAGCTG
TTGCATCGGCCGGTGGTGACAGCGCCGACCACTTGACAGCGCGATGGCGGTGAACGGTGACAAGGTGAGCTGCACC
CCGCCCGCAATGCCACGTGCGTTTCACGCAAGCGAAGCTTGACACGCCAAGTGAATTGCCACCAGCGACGACGAAC
AAGCGGTATCTACGGCGATG (SEQ ID NO. 318)

Clone Rv273

:::Rv273SP6.seq:::

GGGTGCACTTTCTGCAAGGCGAGGCTACACCGTCGTCGTTGATGCGATAGCCATCCCGTGGGCTACTCGCCAT
CACCGATCAGCTTCGCCCCGAAGCCGCGGTGATTTCGCTGCGACCAAACCTGAACGGGGCCAAACCGGTATTGCT
TACCGGCGACAACCGGGCCACCGCGATCGGCTCGGTGTTTCAGGTTGGCAT (SEQ ID NO. 319)

:::Rv273T7.seq:::

AATCCGAAATCCTGACCGATACTTGAACTGGTCTCGTTCCGCAATAACTCGTCGGCGTGACGAGCGCGCGCAAACG
TACTTCGGCATCAACCGCTCCGACCTGAATTGGCAGCAAGCGCGCTGCTGGCCGGCATGGTGCAATCTAACAGCACG
CTCTTCCCGTACACCAACCCGACGGCGCGTGGCCCGGGCGGAACGTGGTCTCGACACCATGATCGAAAAACCTTC
CCGGGAGGCGGATG (SEQ ID NO. 320)

Clone Rv274

:::Rv274SP6.seq:::

TTCCGAATTTCCGGTCCNGGTCATATGACCCTCATGGAAGAAGAAGCGGCCGCCCGCGCCCGTGGCAGGCGAATGA
AAACCTCACCGAGCCGCATTGAACGCCGACAAGACGGTGGAGCAGGTGCAAGACGTCCTGGACGGTCTGGGTAAGA

CCATGGCCGAGCTGAACAGCTCGCTGTACAGCTGAACAGCACCGTGGAGCGCTTGGAGGACGGTCTGGACCATCTCG
AAGGTACCCTGCACAGCCTGGACGATCTCGCGAAACGGCTCATCGTGTGGTTCGAGCCGGTGAAGCCATCGTCGATC
GGATCGACTACATCGTGAGCCTCGGCGAAACGGTGATGTACCGCTGTGGTC (SEQ ID NO. 321)

::::::::::Rv274T7.seq::::::::::
NCTCGATCTTGGGGTACGTTTCGATGAGGCTGCTGACCAACCCGGCCAAAGCGGGTGGGACTGGATGGATACGGATT
GCACATCATCGAGCGCGTGCCGCTGCCGGTGCGGGCCAACGCGGAAGAACATCCGTTACCTGATGACCAAGCGTGACA
AATTGGGGCACGACTTGGCTGGGTGGACGATTTTACGAATCCGTGCATCTGCCCGGAGAATTCGGCGGTGCGTTGT
GAAGGTGGCGCCGGGGTGCCGGATCTGCCGTGCTGGATCGTCTGGTGTGCGGCTGGCGATTGTGCCAGCAGCTGGC
ACGGAAGATCTGCGACGCGCTGTTGGACGGCGCCCGCAAGTGCCCGCCGGGTGTGGCCTCGATGACCGACTGTGGTT
CGGGTGCTCCGCGCGATCGATAT (SEQ ID NO. 322)

Clone Rv275

::::::::::Rv275SP6.seq::::::::::
TCATCCCGACAAAACGCGAGCTAGGTGCGGCATCCGGGAAGCATCGCGACACCGTGGCGCCGAGCGCGCTGCCGGCAG
GCCGATTAGCGGGCATATTATCCCGCCGCGGCTCCCGGCTCCGAGTACGGCGCCCGAATGGCGTACCGGCTGGTA
ACCGCTCTTGCGCGCCTGGGCGGCGCCTGCCGGATCAGTGGTAGATGCCNACAAAGCCTGCGTGATCGGTATCAC
CAACGGTGACAGCAGCCGGTTGTGACCAAGCGCGAACGCCACCCCGGTCTCCGGGTCTGTCCAACCGATCGACCGCC
CAAGCCCATGAACAAACCCCGCATCACGTTGCCGATCGGCATACCGTGA (SEQ ID NO. 323)

::::::::::Rv275T7.seq::::::::::
TTGGCGGGTGGCCAGCAGCCCGCGGTGACGGCGACGATGCTGGGCTGGTTGCGGCCCTGCGCCACCGCGGCTTGC
ATGCTGGTTGGCTGTCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGTGATTTTGGGGCTACCGCGATTACC
CCGCGCGGCTCGACGAGTTTGGCCTGGACTACCGCGTGGCCAATCTGCTGAATCGCGGGCCGGTGGTGGCCTGGA
ATGTCGAGCGCCGTTACCTACGTGACCTGATGGATCGGGGGTGCCGACCGTGCCCGGCGATGTGTATGTGCCGGAN
AGCCGGTCCGGTTGCCACGCAAAGGCCATGTCTTCGTGGTCCGACCATCGGTACCGGGACACGGCGCTGTATTGCC
GGTTCGCTGCCGAGTTCTGTCGCGCAACTGCACGCGGCGGGGCCAGCGGTGCTCGTTCCANCCGGAGGTTCCGGTGACG
ATGATCGTGTGGTCTCCCT (SEQ ID NO. 324)

Clone Rv276

::::::::::Rv276SP6.seq::::::::::
GTAGGAGAGAAACAAAGACCGTCGATAGGACACGTGTTACGCCGGTAGCTGTCTTGGTATGGGGTCCGCTGCCGGGG
GGCATCTACTACCCGATCGGTTGTGGGAGGCGTTGCTGCGGGGCGACAATCTGGTCACCGAGATCCCCGCCGACCGC
TGGGACATCTACGAGTACTACGACCCGAACCCGGCGTGCCCGGACGCACCGACTGCAATGGGGCGCGTACCTCGAT
AACGTCGGCGACTTTGATCCCGAGTTCTTCGGGATCGGGGAGAAAGAAACGATAGCGATCGATCCGACGACCGCTTG
TTGCTGGAAACCTCCTGGGAAGCCATGGAACACGGCGGGCTAACACCGAACCATATGCCTCCCGACANGGGTTTCGT
GGGTT (SEQ ID NO. 325)

::::::::::Rv276T7.seq::::::::::
CGAACTGAGCCCATAGAAAGGCAGCGACTAATTCGCTGGGCAAATAGGAAGACCCTTTGTCTGCCACGTATATTTGT
CGACCTCGTTGCGAAGGAAGCGGCTGCGATTGGTGCCCTTTTCCCTGGAGAATCTCTGCCCGGAGCAGGAAGTCTTAT
GAGTTGACAAGCAGGGGCGCCGCTTCGCCGGAATCACATTCTTGGTCTCGTGAAATGAGAGCGCTCCAGGTGCGC
GATGCTGCCGAGCGCCCGCCACGATACGACGCCATCGCGCCTTGGGCGCGTCTTCGACCACCGCCAGGTTGTGGTG
CGTGGCGATCTTCATGATCGCGTCCATCTCGCAGGCCACCCGGCATAGTGAACGGGGACCATGGCCTCGGTTGCGGG
TGAA (SEQ ID NO. 326)

Clone Rv277

::::::::::Rv277SP6.seq::::::::::
CTTAGACGCCACCTCCGGGCGGAGCTCCACGGGTGGATAAGTACGGCCGGATGTGGCCGCAATGGGAAGTTGTTGCC
CGCTTGACTGTCCGGTTAACGCCGATTCCACCACATCCCCTTGCGAAAGGCCGTTGGGTT (SEQ ID NO. 327)

::::::::::Rv277T7.seq::::::::::
GATCGCGATCGTCGATGTGGCCATCCGGCTTGGCGTCGACCCGCGTAAGGCAGACCAGATGGTTGCGGGCACGGTCAA
CCTGCCACACGCACTGGTAAGACTGCCGCGTCGCGGTATTGCGGGTTGGTGAAGAGGCCGATGCTGCCGTTGCCCG
GGGGCTGATGCTGTGCGATCGACGATCTGATCGAGAGGATCAGGGCGGCTGGCTGGAATTCGATGCCGCGATCGCGAT
ACCGGATT (SEQ ID NO. 328)

Clone Rv278

:Rv278SP6.seq:::

AGCTTACGCCGCTTTTCGCTTCNGATTTGGGACGCCGCATCGAAAGCGCAGTTGGAAGCGCGGGCGCCCGGCTGGTTCGAG
CTGCTCAAGCAGCCGCAATCCCAGCCCATGCCCCGTGAGGAGCAAGTGGTTTCGATCTTCCTGGGCACCGGCGGTTCAC
CTGGACTCGGTGCCCGTCAAGGATGTCGGCGGTTTCGAAACCGAATTACTGGACCACATGCGGGC (SEQ ID NO. 329)

:Rv278T7.seq:::

CGACGGGACCTCGTCGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTATAAGGTCGGC
GAAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGATGCCCTCGGGTCCNGCCAGCACTCCTCAGG
CTTCGTCGGGGTGGTCGCGACCGCATGGGCCACATCGCATTACCAGGTCTGCGCGAATCACCAGCAGCTANACGGTT
CCTTTCTAAGCAACACCGAAATTTTCAGGACCCGAATGCTCCGGGAAAACATGTACGGTAAGTCCGGTATTCCGGGT
ACCGGTTGAGCATTGA (SEQ ID NO. 330)

Clone Rv279

:Rv279SP6.seq:::

CGGCATCGGTTTGGGCTGTACACGAGTTGGTAGTTCTTCACTACTGTTGTTTCGAGCGTCGAGCCGCCGCGCGTGT
GAGGTCGCCCGGACGCGTACCGCCAGGCGGTGAGGTCGCCCTTCAGTCCACGCNGCTGTGGTCCGGCTAACCGCTTA
TCTTCAATCGAGACNATCGCCAGCTTCATCGTGTGGCGATCTTGTCCGAGGGCACCTCGAACCGGCGCTGCCANTAC
AGCCACGCGATCGTGTGGCCTTCGCGTCGACCATCGTCGATACCGCAGGCACTTGCCCTCGAGCAGCTGGGCCGAT
CCGTTGGCAACGACCTCAGAGGCACGATTGGACATCAGCCCTAGCCCGCCTGCG (SEQ ID NO. 331)

:Rv279T7.seq:::

CCGTCGANGCCGCCGACTTGGCTTGACCGACACCAACATGGCCTGAGGGTGTCAACAAGACCGTGGCCGACGGGGCTG
AACATCACCATTGAGCGGCATGAGCCACGCCACCGAGTTTCATCATGTTGATCGCCGAAAACCATTGGCGGGTAGCGGAA
GAACGGTCGAGGTGCTCTACACCGAGTATTGAAAGTCGAAAGGCCAACCGCTGCTCAACGGCGTCAACATCATTTTCG
ACGGGTTTTCGCGAGGGAGGATGCCACGATGAACTGGATCCAGGTGCTGTTGATCGCGTCGATCATCGGGTTCGCTGTT
CTACCTGTTGCGGTGCGCGCAAGCGCGCGGTCCGTGCCTGGGTCAAGGTGGGCTATGTCTTGTTCGTGCTCCCGCA
TCTATGCCGTGCTGAGA (SEQ ID NO. 332)

Clone Rv27

:Rv27SP6.seq:::

TTACACGNCCTGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGAC
CATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTTTTCGAGCGTCGCGCGGGGAGCTTCGCCGG
CAATTTCTACTAGCGAGAGTCTGGCCGATNCGGATCTGACCGAAGTCGCTGCGGTGCAGCCACCCCTCATTGGCGAT
GGCGCCGACNATGGCGCCTGGACCGATCTTGTGCCGCTTGCCGACGNGACGCGGTANGTGGTCAAGTCCGGTCTACN
CTTGGGCCTTTGCGGACGGTCCCGACGCTGGTCGCGGTTGCGCCGCGGAAAGCGCGGGTCCGGTGCCATCAGGAATG
CCTCACCGCCGCGCACTGNACGGCCAGTCCCGCGCGCATGTGCGCATCGGGACATCATGCTCGCGTTCATACTCCT
CGACC (SEQ ID NO. 333)

:Rv27T7.seq:::

CAGGCATGCAAGCTTTGTACACCAAGTGTTCGACCAGGCGCTCCATCCGGCGAGTGGATACTCCCAGCAGGTAGCA
GGTCGCCACCACGCTGGTCAGTGCGCGTTTCAGTCTGCTTTCGCGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTG
GCGCAGCTTGGGATCGCGACGTCGATGGTTGCGGCACGGGTGTCGAAATCACGGTGGCGGTAGCCGTTGCGCTGATT
GGACCGCTCATGCTGCGTTTCGCGGTAGCCCGCCCGCACAGGGCGTCCGGCTTCAGCCCCCATCAAGGCGG

(SEQ ID NO. 334)

Clone Rv280

:Rv280SP6.seq:::

AGCTTAGCCAGTTTTTCTACTCTTGGGCCACACCCACAGTGCTTCGACGGTACGGTCACCCATGATGGCCATCCAGT
TGGCATCGGTGAGCTGATAAATGCCAGCTGGTTTCGCCAACC CGGTAGCGATCTTGGCGCGCTGCTTGTGTCACTGA
TACCTATCGAGCAAGACAGCCCGGTTTGCACAAGATGACTTTTCGGATCTCTTCGGCGACTTCGATGGGGTTCGTTCGG
GAGTCCCGGGCGCCACCGGAGGTAAGCCTTCGTCCAGCCCCATACCTCGACCGGGTATCCAGGTTCGCGCAATAACG
CCACCACCTCCTCGGACGCCGCGTTGTAGGCGGCTGGGTTTCAGCGCAAGAAGTGGCCTCAGGGCATCGTCGGCGCGG
TCCCAACGGCNTGCCGGCGGCACACCGTAGGCGCGGGGCTC (SEQ ID NO. 335)

:Rv280T7.seq:::

CCGGCGGAACTCAGACGTGCTGGTGGTGCGGCATGGCACCGCGGGCAGCAAAGCGCACTTCTCCGGGGACGACAGCAA
GCGACCGCTAGACAAGAGGGGTGCTGCGCAGGCAGAAGCGTTGGTACCACAGCTGCTGGCGTTCGGCGCCACCGATGT
TTATGCCGCGCGAGGTGCGCTGCCACCAGACGATGAGGCCACTCGCCGCGGAACTGAACGTGACCATAACAACGA
GCCACCCTGACCGAAGAGTCTACGCCAACACCCCAAACGCGGCGGACACCGAGTGCTGCAGATCGTCGAGCAAGT

AGGCACACCCGTGATCTGCACGCAGGGCAAGGTCATTCCCGATCTGATCACGTGGTGGTGCGAGCGCGACCGTGTGCC
CCCGACAGTCCCGCAATCGCAAAGGCAGCACGTTGGTGT (SEQ ID NO. 336)

Clone Rv281

.....Rv281SP6.seq.....
GTATGGTCAGCTGTCCATCCGGCGCTGTCCGGCCGAGCTGCCAGATCTCGTCAGCCGTAACCGGGTTGCGGGATCCACG
CGTGCGGGTTGTCTAC (SEQ ID NO. 337)

.....Rv281T7.seq.....
CCGACTTTCGCGGGTACCCGCTCAACTTTGTGTCNACCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACT
ACTTCATCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACT
ACATCATTCGCACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACC
TGGTTCAAACCAACTTGAAGGTGATTGTTAACTGGGCTACGCCGACCCGGCCTATGTTTATTCGACCTCGCCGCCCAA
TGTTGCGACTCCGTTCCGTTGTTCCAGAANGTCAGCCCG (SEQ ID NO. 338)

Clone Rv282

.....Rv282SP6.seq.....
GCACCGATGTCGGCGAGCACTTCGTCAACTTCCAGGGGTGCCCGCACCAAGTATTTGACGAGTATTTCCGTCGGGCC
GCCGCGCGCGGTGCGCGGCAGGTGGTCATCTGGCGCGGGGCTGGGACTCGCGCGCGTACCGGCTGCCTCGGC
(SEQ ID NO. 339)

.....Rv282T7.seq.....
TGCACCCAACCTTACTGAGCATGCTAACGCTGGTTCGTGCGGGTCTTGTTCGCGGTGTCGGCAGGGCACACGCTCGGGG
CGTAGCTGGGAGAGGCCCCGGTCAAGCCCGGAGAGCAGTGCTCAGTCCGCCAGCTTGACCGACTTTCGATGAGAACGC
GCTTCTCGCCGTATTGAACTGGCGTGCTGACGGTTCGTGAGCAGCGCTCGCCGAGTGCGGCCGCTGATTCTTTCATCG
AGCCAGGACGCGCATTCGTGTTCCGGCCGC (SEQ ID NO. 340)

Clone Rv283

.....Rv283SP6.seq.....
AGCTTACGGCCGGTCGACGCGACGAGTGTTTCATGACACCACAAACCGTCAACGCCTACTACAACCCGGGGATGAACG
AAATCGTCTTCCCGCAGCGATTTTACAGCCACCATTTTTCGATCCGCAGGCCGACGAGGCCGCCAACTACGGCGGGAT
CGGGCGCGTGATCGGGCACGATGATCGGGCACGGTTTCGACGATAGGGCGCCAAATACGANGGCGACGCAATCTGGT
CNATTGGTGGATCGA (SEQ ID NO. 341)

.....Rv283T7.seq.....
ATGTCGTACGTCACCACAATCGCGAGGACCCAATCATGCCGCCAGGGCGGGCAACCCAATGGTGGCCGCGAAGCGG
CAGCTCGATCGCAGCGCGGAGGTGCCGCCGCCAGTTGATTCACGAACAGGGTGAGGTATAGGCGGGCAGGATAGTG
ACGAACGCAAGACCTATATCTGCCGTCCGAGTAAGAATCGAGTAGCCGGTCGACCAACGGAAGCGAAAGTGTCCGCGA
TGTTGATGAGCGTCGCCGTTGTGGCGCGGTGGC (SEQ ID NO. 342)

Clone Rv284

.....Rv284SP6.seq.....
AGCTTACCAGCGTGCCGATGCTGTTCGCNACACCTCCCTACTATGCGCAATTGCCGACACGGGTGGCATCAACACG
GGCGATAAGGTGGACATCGCTGGGGTGAACGTCGGGCTGGTGCCTCGCTGGCAATCCGCGGCAACCGCGTGTGATC
GGATTCTCGTTGCCCGGCAAGACAATCGGGATGCAAAGCCGGGCAGCAATTGCAACCGACACCATTTCTTGGCCGTAAG
AACCTGGAAATCGAACCCTCGGTTCCGAGCCGTTGAAACCAACGGTTTCTGCGGTTGGCGCAGAACACTACGCCA
TACCAATCTATGACGCGTTCGTC (SEQ ID NO. 343)

.....Rv284T7.seq.....
CTGCCGCGGTGGCGGTGAGCGCCTGGCAAGTCACCGCACCGCGCTCCGGTTCATCGGCAGGCTCCCCGAAAAGGGCC
CTGGCAACAGAAGGTGATCAATGAGCTCCCGCAGACCTTCGCCGATCTGGGACCGACATACGTGAAGTTCGGCCAGAT
CATCGCGTCCAGCCCGGGAGCATTCGGTGAGTCGCTGTGCGGGGAATTCCGCGGCCCTGCTCGACCGGGTGCCGCCCG
CAAAACGACGAGGTGCACAAGCTCTTCGTGAGGAACTCGGCGACGAGCCGGCCCGGCTGTTTCGCCTCCTTCGAGG
AAGAACCCTTCGCGTCTGCGTCCATCGCCCAAGTGCCTACGCGACCTGCGCAGCGGCGAAGAAGTGTGGTCAAGATC
CACGGCCGGGCATCCGCCCGCGGTTT (SEQ ID NO. 344)

Clone Rv285

.....Rv285SP6.seq.....

GATCGTGCCGGCCCCCGGGCGGCGAGTAGCAGATCAGCTCGTCGAAATCGCGGCAACCAAGTCCAGTTCGATTCCATACG
GGCGCCGTCAATCAACTCTGCGAACATCGCGATCGGCACCGGAAACCGGCGAGCCGCTCAGCCAGCGCAACCAAGCAC
CGGGATCGGATGAATCATCAATATTATCAAGTGATTCTCTGATGGCATCGAGCTCGGTGATCTTGGTCTCGGGGGCCA
GCTCGCGCTCGGCGACGTCGTCGATCCGGCGGGCGAGCGCATAGACCGCAAATAGTGCCGCTCGCTTTTCGGCGGGCA
AGAGTCGGATGCCGTAATATANGTTTCTGGCGGCCGTGCGCGTGATCNACTCGGTGATTGATACGCCTGTTTCATCTC
GGTCATGCCGTCCTC (SEQ ID NO 345)

.....Rv285T7.seq:.....
GGTGGCGCAATGACCGAAACACCCAGCCCGCAAACCCGGCGGCCCGGGCGGCCCGCACAAATCGTTCGTGTTG
GAGCGGCCCATCCAGACCGTTGGGCGCCGTAAGGAGGCCGTGGTACGAGTGCGGCTGGTGGCCGGCACCAGGCAAGTTC
GACCTCAACGGCCGAGCTTGGAGGACTACTTCCCAAACAAGGTGCACCAAGTTCGATCAAGGCACCCCTGGTCACC
GTGGATCGGGTGAAAGTTTCGACATCTTTGCCACCTGGGCGGCGGCGGCCCGTTCGGGTTCATGGCCGGCGCGCTGCG
CCTGGGTATCGCCCGGGCATTGATTCTNGTATCGCCGGATGACCGGCCCGCGCTGAATAANGCCGGCTTCTTGACCGT
GATCCACGCGCCACCGAACGCAA (SEQ ID NO. 346)

Clone Rv286

.....Rv286SP6.seq:.....
CACAAATAGATTACTCAAGCTTCGAACAGCGGCCTTATCACGTATCCCCGCTGAGACCTTGACCCTTAGGGCCGAAGT
GACTTCGCTGCTGCTATGCCGACACCCGATTTCCAGACGCTGCTGTACACGACGGCCGGGCGGTGGCCACCATCAC
GCTCAACCGCCCGGAACAGCTCAACACCATCGTCCCGCCATGCCGACGAGATCGAGGCCGCTATCGGGTTGGCCGA
GCGCGACCAAGACATCAAGGTCATCGTGCTGCGCGGTGCCGGCCGCGCCTTCTCCGGCGGTTACAACCTTCGGCGGCGG
GTTCCAACATTGGGGGCAT (SEQ ID NO. 347)

.....Rv286T7.seq:.....
TCAGGACGCTTATGGTTGGCAGATGGTGGCCTGGCGTCAATACGCGCGAGCGCATGAGCTCACCGGTTCCGGAACAA
CGTATCGAAGAAGCTCGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTATCCCAACTCTAACTGTGCT
ATCGGATCAGCGTGAATATCGAGATATTGCGAATGCGATGACAGGCCGCCATTCCGTTTATTCGCTTACGCTTCCCGG
GTTTCGATTGCTGCTGATGCACTGCCGCAAAACCGGATATGATTGTTGAAACCGTATCTAACGCAATTATTGATGTGGT
AGGCGGCAGCTGCCGTTTTGTGCTGTGCGGCTATTTCATCGGGTGGGGGTGTTTGGCTATGCCCTCTGCTCCCAT
(SEQ ID NO. 348)

Clone Rv287

.....Rv287SP6.seq:.....
CGCAGCTGTGCGCGATCTGGTCCGGAATACCTAGCTCCAGGTTCTGAGTGGAGATGAGTGCGGCCATCGAAGTGTTGT
CAATGTACTCCAGGATGTGAGGTGCCAGGCCGTGGCGAGGATCTTGGGCACCGCCGCCATGACTTGGTTCGAAGTCGG
CGAACGGGGCGAGCACGCTGGCGTCTGTTG (SEQ ID NO. 349)

.....Rv287T7.seq:.....
GTAGTTCGTTTCATCAAACACAGTGCGGTACCGGTCAAGCGGATCACCGACTTCACCGGGCGCGATCCCAACCCAGCC
ACGCGATGCCTATGTCTTCGGGTGGCGGCCACCGTGGGTCAACTCAACTATCCGACGCCGCACTGAAGCATCGACAG
CAATGCCGTGTATAGATTCCCTCGCCGGTCAGAGGGGGTCCAGCAGGGGCCCGGAAAGATAACAGGGGCGCGGTC
GGACCGA (SEQ ID NO. 350)

Clone Rv288

.....Rv288SP6.seq:.....
TCCGCTCGCTTCTCCGAGAGGTTGAGTGCCAACGCTCTGCCGATGCCCGAAGCCGGCCCCGGTGATGACGGCGACCTT
GCCTTCGAATGAGCTCATTTGACTACTCCCCGTGGTTGTCCCTGCGATTGGTGGAGGTGGCCGCGCAGCCTTGCCCCG
AGGTCCGGCGATCGCGTCTCGGGCTTCGGGGAGCAGACTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCAACCCG
CGATGCTCGATGCTTGTTCGAAGCGGCGCAGGCGGTTTCGATCTTGTCCGCTCAACACNGATCGGATCGTCGCC
CGGCTCTGCATGACGAATGGCG (SEQ ID NO. 351)

.....Rv288T7.seq:.....
ATGGGAGGCCACCGATTACCATCTTGACACACCGATTCCGGGCTATTGATGTCCACGTTCCGGTCCGCGAACCAGCGCT
GTGGCTGCTGCTGGCCAAAGGCGGAGGCGATACCGAAGTCAGTGCCCAAGCTTGGGTTCCACGCTCGCGCAGCCACCGC
CGTCACCTTTCCACGAGACCTCACCTGCCGATCCGAAATGGAATCGGCCGTGACGGAATTGGCGCAGCGAACACTCAA
CGAGGTGGTGGCTTCGTGCGAACCCTCACCCGATCGCGGTACCGTGCACGCGGACGTTCTACACCCGCAACAA
GATCCGAAAGCTGCAAGCTCCAGCACCAGTCCCGACGTCATCACCGCTGCCGCCCGGACGTTCTTGAACCTATTCCG
AGCTGGAATCGGCCGTCCGGTTGCTGGGAATTGCNGTTAAGAAGTGGGCT (SEQ ID NO. 352)

Clone Rv289

.....Rv289SP6.seq:.....
GCTTTGCGCGCTTCTCCGAGAGGTTGGAGTGCCAACGCTCTGCCGATGCCCGAGCCGGCCCCGGTGATGACGGCGACC
TTGCCTTCGAATGAGCTCATTGACTACTCCCCGTGGTTGTCCTTGCATTGGTGGAGGTGGCCGCGCAGCCTTGCCC
CGAGGTCGGCGATCGCGTCGCGGGCTTCGGGGAGCAAACCTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCAACC
GGCGATGCTCGATGCTTGTTCGAAGCGGCGCAGGCGGTTTCGATCTTGTCCGCGTCAACGCAGATCGGATCGTCGCG
CGCGGGTCTGCATGAAGAAT (SEQ ID NO. 353)

.....Rv289T7.seq:.....
CTCACGCAGCCACGCCGTACCTTTCACGAAGACCTCACCTGCCGATCCGAAATGGAATCGGCCGTGACGGAAATTG
GCGCAGCGAAACACTCAACGAGGTGGTGGCTTCGTGCGGAACCGTCACCCGAGTCGCGGTACCGTGCACGGCGAC
GTTCTACACCCGCACCAACATCCGAAAGCTGCAAGCTCCAGCACCGATCCCGACGTCATACCGCTGCCGCCCGCA
CGTTCTTGACCTATTTCGAGCTGGATCGGCCCGTCCGGTGTCTGGGAGTGCGGTTAGAAACTGGCCTAGAAACCGGCGG
GCACACCGCACCTGGGCGGGN (SEQ ID NO. 354)

Clone Rv28

.....Rv28SP6.seq:.....
TGCTTCCGGCTCGTATGTTGTGTGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTAGGTGACACTATAGAATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACC
ACNCGCGGGTCGGGCGCCGGGCCCGGGTCGCCANGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCCGGC
TGGCTACGTCGAGCCATACCGGGCGAGCTACATCGGCTCGGCCGCCAGTGTTTCGAGGCTTCTTCGAAGTCGAAG
TCGATACCGATTGCGCATCCGCGCCGCA (SEQ ID NO. 355)

.....Rv28T7.seq:.....
CAGGCATGCAAGCTTACGTCCTGACGGCTCGGGTACGCTTCGGTTCGCAGTGTGCGAGTGATAGATGACGACCGGGAC
CTCGTCTGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTACCCGGAATCCAACCGGTAGAAGGTGGCGAGCGCTC
GGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAGAACCTCGGGTCCGGCCAGCACTCCGCAGGCTTCGTCCGG
GTGGTTCGCGACGCGCATGGGCCACC (SEQ ID NO. 356)

Clone Rv290

.....Rv290SP6.seq:.....
GCTTGTCTATCGTCCCGGCCAGGTCCGGCCAGTCAAGGTGCAAGGCCAGTCCGGTCTCTCTCCGACTACGGCCAAGA
ACTGGGCGACGGTGTGAGTGCAGACCAGCGGAACTGGTGGCGCCCTAGGCGAGCGACCGCCTCACAACGGCGGTGA
CCGCGTTCTGGTCTGTCAGCATCGAGCCGTGCCAGCCCGCGCGTCCGTCAGCCGCATCCACTGGATGCCCTTCT
CGGCGGTTTCAATCAGGTACAGGCGACGTTCCGCCACCATCGTGCCGGGGCACGGTTAGCGAGAAACCGCCGACTTCAC
GATTGCCTCGGTGATGCCGTCGAAACAGATCGGGCCT (SEQ ID NO. 357)

.....Rv290T7.seq:.....
GCGCGCCATGTTGAGGTTGTCCGACGGTGACGACGGTGAACCACAACCTGTTTGACCTGTCCGCACACACCGTGTGGAT
CGGCGAGCGGACCCGACAAATCGATGGCGCGCACATCGCGTTTGCCAGGTGATTGTAATCCGGTCCGGGTCAAGTT
GGGCCCCAACATGACCCCGAACTGGCCGTGGAGTACGTGAGCGGCTCGACCCGCACAATAAGCCGGGCCGGCTGAC
TTGGTGAGCAGGATGGGCAACCACAAGGTCCGCGATCTGTTGCCACCGATCGTGGAGAACGTCCATGCCACCGGGCAT
CAGGTCATCTGGC (SEQ ID NO. 358)

Clone Rv291

.....Rv291SP6.seq:.....
TTGCCTTCCATGCCGAGCAAGGTCGACTCAGCGATGACGAATTGTTCTTCTTCGCGGGTGTGCTGCTGGTTGCGGGC
TATGAGAGCACTGCTCATATGATTAGCACATTGTTTCTGACGCTGGCCGACTATCCAGATCAGCTGACACTCCTTGGC
CAGCAACCAGACCTGATCCCGCCGGCGATCGAGGA (SEQ ID NO. 359)

.....Rv291T7.seq:.....
CGACGCTGGGCCCAACTGCGACCACAGGTCTGTTATGGCAGGACATGGCCGGGTTTCAGCGGCGCCAATACCG
(SEQ ID NO. 360)

Clone Rv292

.....Rv292SP6.seq:.....
TAACGACTCGGGTCCAGCGACCGCGCCAACACNAACGGCCGACNACGTGGGCCAGGGTCGCGGCCTCCCTACAAAC
AGGATCCGTTGCTTGCAGACAGAGGCTCCGGTGGCGGCTTGGGCGCCGTGCTCGTCCAGCGTCCGGTCCCGGGTGC

CCGGCGACGCTTGTTTCTCCATACTCGCCCCCTAATCTCGAGGCAGCCCGTACCCGCAGGCAACCTCCCAAAATGC
AATCCCCCAAAATGCAATGCGTCNAGCTATTTCTCACACCGACCGCTAGTTGCGGATCANAAATCCGTTGGGCGCGGA

(SEQ ID NO. 361)

::::::::::Rv292T7.seq::::::::::

CNTGGCGGTGGGTGCGGTGTCGAACACGACCACACTTCTTTGCGGTTCGGTGATCTCGACACCGGCCGCGAGCCGACC
ACCATGCCGCGGTAGATCGGCGATCAGCGCGTTCGGCTATCGCTGGGTGCCGCCCACCGGAATCGGCCAGCCGACCGA
ATGGGCCAGCGTTGCCATCATCAGTCCGGCGCCGGCCGACACCAAGTGACGGCAACGGTGAAATCNCGTGGGCGGCAAC
GCCGGTGAACAACGCGCGGGCATCCTCGCCCGCCAGCGACCGCCAGGCAGGGGTGCCCTGGGCCAGCATCCGCAGCCC
GAGACNCAGGACCGANCCAGTG (SEQ ID NO. 362)

Clone Rv293

::::::::::Rv293SP6.seq::::::::::

GCTTTTCNGATCGCAGCGAGTCGTACCCGCGCCGGTCACTTCTGTGGATATCGCCGGCCTGGTCAAGGGGGCGTCCGA
GGGAGCCGGGCTGGGTAACAAGTTCCTGGCTCATATCCGCGAATGCNACGCCATTTGTGAGGTGGTGCGGGTGTTCTGT
CAACAACNACTTGACTCATGTCCCGGACGGGTGATCCCCANTCCGACATTGAGGTGCTCGANACCGAGCTGATCCT
GGCANATCTGCAAACCTGGAGCGGGCCACGGGCGGGTGGAGAAGGAANCGCGCACCAACAAGGCGCGCAAGCCGGT
CTACGACGCGGCACTGCGTGCCAGCAGGTGCTCGACGCCGGCAANACGCTGTTCCGCCGGGGGTGGATGCCG

(SEQ ID NO. 363)

::::::::::Rv293T7.seq::::::::::

GTCGTACGCCATTNGTTCGGTGTGCGCATACCAAGTACGACGCGCCGGGCACCTGACGCGGCGGCGCGACCAAGTCGGTG
GCCATCGCCATCGTCTGCCACCCGGTCAACGGACGCACCTTCTCCTGGCCGACGTAGTGCGCCACCCGCGCCCGTTG
CGTCCCATCNATCCGGTCAACATGAGCAGCGCCAACACCGAGCGGTACATGACATCGCTGTGGAACCAAGTGACAGATT
CCGCCGCCCATGATGATCATCGACCGTCTCCGGATTTCGGTTCGCGTTGCGGGCGAAATTCCTTGCAAACCGGATTGC
CTGCGCGGCGCGCACACCGGTGATCGACTCCTGCCAGGCCGGGTGTTCTGCTGGGTTTCGGTTCGTGGTACCGGT

(SEQ ID NO. 364)

Clone Rv294

::::::::::Rv294SP6.seq::::::::::

GCGAGGCGGTATCGCTTCCCGTCTACCGGCGACCGCCAGCCGAGAAGCTCGTTTTCCAGTGTTGCTGGGGATTCTC
ACGCTGCTGCTGANTGCGTGCCANACCGCTTCCGCTTCGGGTTACAACGAGCCGCGGGGTACGATCGTGCGACGCTG
AANTTGGTGTTCTCCATGGACTTGGGGATGTGCCTGAACCGGTTACCTACNACTCCAAGTGCGCGCCGTCTCGTCCG
CAGGTTCGTTGCTTGCGATAGCCGGGAGGCCCGGATCCGCAATGACGGATTCCATGCCAACGCTCCGAGTTGCATGCGG
ATCGAATACNAATTGATCACCCA (SEQ ID NO. 365)

::::::::::Rv294T7.seq::::::::::

TGGGTCTTGCCGGCGAGCCAGCGAAGTCGCTAGCGTGGCCGTGTTTCTTGGCTTCGGATCTATCCTCGTTACATGAC
CGGCACCGTGTTGGACGTGACTGGCGGCCGGTTCATATGACACCGAGATCATTGCCACGGTACGGCAATTTCGTCAAGA
AGGAAATCTTTCCCNATGCACCGGCCCTCGAACGTGGCAACAGCTACCCGCAAGAAATCGTCGATCGGCTGGGTGTTA
TTGGCTTGCTCGGTGCGCGGCTGCAAGGGTATCGACACCACCGAGTTTCATTCTCGGGCGTGCCGGCGCATTCGAGCTG
GCGGTGCGCGCTGCCAGCACCGTCATAAGTACTTGANGATGGTCAAACGTCCGACGAACCGCCACCACGTGCTGCC
GAACGG (SEQ ID NO. 366)

Clone Rv295

::::::::::Rv295SP6.seq::::::::::

TAGATGCCCAAGCTTGCCNTTANAGACCTCGTCGACCAAGCACGGACCGACCGTCAAGGTGGCGAATCCGGGCTTG
GCTCNACCCGCGTAAGGCAGACCAGATGGTTCGCGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGCCCGCG
TCGCGGTATTTCGCGTTGGTGAAAAGGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGCGGAGTGACGATCTGA
TCGAGAGGATTACAGGGCGGCTGGCTGGA (SEQ ID NO. 367)

::::::::::Rv295T7.seq::::::::::

TCTCCACGGCGTGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCTGCGTTAG
CGCCGGATTCCACCACATCCCCTTGCGAAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCCATCGAGATAGTGG
AGCAACGCAATCCGTGCGGTACGGTTCGGGTGCTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTCTATTG
CGCGAAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTNGGTAATCCGGCC

(SEQ ID NO. 368)

Clone Rv296

.....Rv296SP6.seq:.....
GCCCGGTTTCGATCGGGCATGTCCGCAGTCGTGTTACCGGAGGCGGTCTGGCCGCGCTAATCGGCGTTCGGCGCCGAC
AAGATGTGGGATATCCGCAATCGGGGCGTCATCCCTGCGGGCGCGCTCCCCGCGTCCGAGCCTTCGTGACGCAATC
GAGGCAAGTCACGACGCGGATGAGGGGACGAGTGAATTACAGCGAGGTCGAGCTGTTGAGTCGCGCTCATCAACTGT
TCGCCGGAACAGTCGCGGACCGGGTTGGATGCGGGACCAACCCCTACGGGGGATCTGCTGTCTCGGGCTGCCGAC
CTGAATGTNGGTGCGGGCANCGCCGTATCNACTCCCGTGGAACACAGCCGGGGC (SEQ ID NO. 369)

.....Rv296T7.seq:.....
CTCGGCGTGGATATCGGTGTAGCCGGCGCCGGTGAANGTCGGCTCCTTACGTCCACTCGACAACAGCTCATAGCGATC
CAACCAGTANGCAACCGCCTTCAGCAGTACAACCGCGCCGGCGAACACTGCGAGTTGAACGCGAGCTGCCTGGGTGAG
CATGCCTCTGCCGTTGTGAGCCGAAGCCGCCGAACAGGTAATGCGTCAACAGGCTCGCTAGAAACGCCAGAACAC
GGCCACGAACAGCCAGTTGAGCACCGACCGGTAGAAGCGGAGATCGAAGACGAAAAACCAATGTATAGCCGAATT
CGGGGTCCACGATGCCAAAGGTGCCCCGTGTACAACAACTGAACCTTCACCCA (SEQ ID NO. 370)

Clone Rv29

.....Rv29SP6.seq:.....
TCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAA
GCTATTTAGGTGACACTATAGAATACTCAAGCTTCACGTCCGTACGGCTCGGGTACGCTTCGGTTCGAGTGTGCGAGT
GATAGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCGCCACACCTTCAGTTGCTCACCAGGAATCCAACCGGT
AGAAGTTCGGGAGCGCTCGGCATTGGTCATCGGGATATGCCGTTCGGGACGGTCAGAGCCCTCGGGTCCGGCCAGCA
CTCCGAGGCTTCGTGCGGGTGGTCGCGACGCGCATGGGCCACCATCGCATTACCAGGTCTGCGCGAATCACCAGCA
CGTAGACGGTTCCTTTCTAAGCAACACCGAAGTTTCAGGACCGAATGCTCCGGGAAACATGTCA (SEQ ID NO. 371)

.....Rv29T7.seq:.....
CAGGCATGCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCCCGGGTTCGGGCGCCGGGCC
CGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGCTGCGCTACGTTCGAGCCATACCGG
GCGGAGCTCCATCCGCTCGGCCGCCAGTGTCCGGGCCCTC (SEQ ID NO. 372)

Clone Rv2

.....Rv2SP6.seq:.....
CCTGCATCCGGCTCGTATGTTGTGTGGAATTGTGANCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTA
CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCCAATCCCCCTGCCCTGATACGCGTCGGCAACCGTGAA
CGCGATCTCGGCGACCGTCGGATCGGTTTCATCCCGCACAAAACGCGCGTCGGCTACGGGGTTCGTTCCGTCGGTCAC
CACCCAGACGAAGTGGTCGACGTAGTCGACTCCGACAGGTAGTGATCAACGCCGACTGGGAACACNAGCCGACAT
GAACCGTCGATACAGCGTCTCNCCGGAGAAGTGGATGTGTCGCTGCACGGTCCGCTCGCGGTACCCGGGACGACGGG
GCGTAACATCAGTTGAGTCCCGTCGGCAAGCCGTACCGGAATCGGGGAGACGA (SEQ ID NO. 373)

.....Rv2T7.seq:.....
CAAGATGATCGCCGTCGCCACCCGATCCGTGCCTCGGTTCAGCGCGAACGTGCTTTCCGGTTCGGGCGACCAACATGTC
GCACGCACCGACAGGCCGAACCCGCCGGCCGCACATGCCCGTTGATGGCGCCGACCAACCGGCAGCGGCGACTCGAC
GATGGCGCGCAACAGCGCCGTCATTTCCCGCGCCCGGCCACCGCCATCCGGTACGGATCACCACCACCAACCGCCGC
CTCGCTGAGGTCCGCGCGCGCGCAGAACGTTCCGCCGGTATGCCCCAGCACGACCAAGCCGACCCGCCGATCTGCTTC
GGCCGCACTCAGCCCTTGATGTAGTTGGCTGACCAGCGTGCTCGACAGCGGTTGCGGTTGTGCGGAGAGTTAGTGT
CAGCCTGGCGAAGGGGCCGCCGAGGCGCGGGCCAGCGTAGTCGACGGGGCTG (SEQ ID NO. 374)

Clone Rv301

.....Rv301SP6.seq:.....
CTCAAGCTTCGATCGACAGTACTCCCGCCTTGGGTCTGGTCTTCGAGCTGGTCGGTCATGGTCGGACCTGCTGGTAGT
GGGGATCTAACGCAACATGTCGGGATTCATCATGGTGTACCCGTGATACCCATTTCGAGCTGCCGGTGAAACCCCGC
GATGCCGGGATTTCCAGCCGCACTAGGATGTCTAGCCGGCCAGCCGCTGCCGCCGACTTCGGGATGTTCCGGTATACC
ACCGATCGGCAATCTTGCNTATCCGCCGATGCTCGAACGCTAGCCACCCCAAACCAACCACTGTGACNACAATC

.....Rv301T7.seq:.....
TGAATTTCCCGATCCCAATCTCGGTTTCAGATACAGGTTCGCCATACCCCTTACTTCGGCAACGCTGGGCGGATTGGC
CCTGCCGCTGCAGCAGACCATCGACGCCATCGAATTGCCGGCAATCTCGTTCAGCCAATCCATACCCATCGACATTCC
GCCGATCGACATCCCGGCTCCACTATCAACGGAAATTCGATGTGCGGAGTTCGTCGGATCGATGTGTCCGTTCGACAT
TCCGG (SEQ ID NO. 376)

(SEQ ID NO. 375)

Clone Rv302

.....Rv302SP6.seq:.....
TACTCAAGCTTGAACGCTGCGAGCGAGCCCATGTAGAGCGTTTGGTACCAAACCGATCGGTGGGCCAACTTGCCATGG
GCTCACAGCGGCTATCGCGAGCGTGTAGCCGATCATCGGCCAGGCGACGGTGGCCTGAGCGGCAGGGGTTGCCTTATC
CATCCTCTTGCGGCATGGTTGCCGAGGGAGTGCCGGTAAGTCTGGTTCGGCAACCTGGCCCGCTGCGGGTTGGGTTTCG
GATTCCTTCGGCTAGTAAGGTGCTCGCCTGGTGTACAAACGAATCGCTAGACAGCTCTTATCGGGAGTGGCCGTCGCG
ATCGTTGCGCTGCCGCTGGCGATCGCGTTCCGCGNTTACCGCCACCGGAACGTCCCAAGGTGCGCTCATCGGGCTCTAC
GGCGCCATCTTCGCCGATTCTTCCCGCCGTTGTCGGTGG (SEQ ID NO. 377)

.....Rv302T7.seq:.....
GCGGTGTCTGAAGTTTCGCCCGTTCCCTCCAGCGCATTGAGCTTCAGCCCGACCGGCAGGTAGGGAGTCCGGCATGCGGT
CCTTCGCCCCGACCCCGCTGGCTAAATAGCCACCCCGAGCGCGGTACGGTCTTTGCACCGGGACGACGGCATACCG
GCAGCGGAACATCGCCCGGGCTGCAGCGTGAACGTCGAATACGAGTCGAACAGTGTGCGCGCGTAAAAACCCGAGC
CGGCGGTGGCTTCCGTAATCAACGGCTCCTGCGCAACCAGCTGCAANTCNCCGGTGCCACCGCGGTTGACAATCTTGA
TNTCGCGACCTCGCGCACCAN (SEQ ID NO. 378)

Clone Rv303

.....Rv303SP6.seq:.....
TACTCAGCTTCGGCTCAGGTGGTGTCTGGTAAAGTTTNCCTGAACGGTGCAGGTTTCGACAATGTGGTGCCGGTTTCG
GCGGTACTGCCATCGAGACTGGCGCAGGCTATCGCACCCGTTATCGGCTACAAACAAATCGCGGTATGCGTTCTT
GAGCATGAGTCGGCGACCGTCGTTCATGGTCGACACCCACGACGGAAGACGAGATCGCCGTCAAGCNTGTGTGCCG
GGATTATCAGGACTGACCTCTGGCTGACCGGCGTGTGGTTCNCATGCCTGGCGCCCGGCGCGGT (SEQ ID NO. 379)

.....Rv303T7.seq:.....
CATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGG
TCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACGAACG
ACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACANCGGTTCTCCACCGACCGGGCCCGGTTGTGG
GGTGT (SEQ ID NO. 380)

Clone Rv304

.....Rv304SP6.seq:.....
CTCAAGCTTCCCGCGCGCCAGTACCGAAAGCGCGAACAGCTCGCGGCAGCCCAACNTGCTGCGTCGGATTGCCGGC
GGCGANATCAATTCCAGGCAGCTCCCGGACAATGCGGCTCTGCTGGCCCGCAACGAAGGACTCGAGGTACCCCGGTG
CCCGGGTTCGTGGTGCACCTGCCGATCGCACAGGTTCGCCCAACACCGGCGCTTGATGCCCGGTGCGCAAGCCCGG
AGTTGCCAAACCCAGCGTGATCAGGCTCGGCTCGCGAGTTTCGGCGAAGAAGTGGCTCGCCTGATCACCTACCATCGGC
CAGGATCTGCGTGTATCACNACGCTCGCCAAGGAGGTTGTTGTGGTGT (SEQ ID NO. 381)

.....Rv304T7.seq:.....
GCCACGTTTCGCGCGCGCCCGGCATACGGCGGCGTACCGATCTCCGCGTCATACCCCGCGGGTAATCGCCGACGGTGC
CGTTTCGCGAGCCGAAGGTGACGACGCTGATTGAATCGAGTTCAGGTCAGCGGGTGGCGCAGCAACGGCGCGAGCT
CAACGACGTCAATCAGTTGTGCTTTCTACGGTCACCGGTGACCGTAGTCGCCCGGTGCGCTCGGCGAGAA
GTTGCACCGCCACACCGCGACACCGTCTTGACGCGGACGCCACCCCGGATCGGTTGTTGGCCAAGGTAATTGGGT
CATTCATTTGACGGGACGCCGACCCCGCAGCCCCAGTACCGCCACGACCACGCGGCTGACCCCACTGTACGA
ACACCAAGGCGACGCCGACCA (SEQ ID NO. 382)

Clone Rv306

.....Rv306SP6.seq:.....
CTCAAGCTTGATGCCGCTAAACCGAAGCGTGAGCACGCCGCCACCCACCACGCGCGGGTTCGGGCGCGGGCCCGGGC
CGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACACCCGGTGCCTACGTCAAGCCATACCGGGCGGA
GCTACATCGGCTCGGCCGCCAGTGTTCGGGCCCTCTTCGAGGTCNAGGTCNATACCGATTGCGCATCCGACGCCG
CACCTGGACGACAGAACCCTACGAGTGCTTGTGCGGCGGGGCCAAAGAACANCTTGGCATCTTGGCGCGATT
GGCCGGCGCGGTCTGGTC (SEQ ID NO. 383)

.....Rv306T7.seq:.....
CTCGGGTACGCTTCGGTTCGAGTGTGCGAGTGATAGTACGACCGGGACCTCGTCGGCATCTTCCATAGCCCGCCAC
ACCTTCAGTTGCTCACCGGAATCCAACCGGTANAANGTCGGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCG
GGACGGTCAGAGCCCTCGGGTCCGGCCAGCACTCCGAGGCTTCGTGCGGGTGGTTCGCGACNCGCATGGGCCACCATC
GCATTACAGGCTGTGCGG (SEQ ID NO. 384)

Clone Rv307

.....Rv307SP6.seq:.....
CTCAAGCTTCAATTCTCCACGACGCTTCCCAAATGAATTTCCCGATCCCACAATCTCGGTTTCAGATACAGGTCGCC
ATACCCCTTACTTCGGCAACGCTGGGCGGATTGGCCCTGCCGCTGCAGCAAACCATCGACGCCATCGAATTGCCGGCA
ATCTCGTTACGCCAATCCATACCCATCGACATTCCGCCGATCGACATCCCGGCCCTCCACTATCAACGGAATTTTCGATG
TCGGAGGTCGTGCCGATCGATNTNTCCGTCNACATTCCGGNGGTACCATCACCGGCACCAGNATCGACCCGATTCCG
CTGAACCTTCGACGTTCTCAGCAGCGCCGGAACCA (SEQ ID NO. 385)

.....Rv307T7.seq:.....
TTAACCCCGTGGCCTCTACGCCGCTNCGGGTCGAACATGCATCCCAGCANATGCTCGAGCGCGCACCCCACTCGC
CGATGGCCGGAACCGGCTGGTTACCCGGGTGGCGGCTGACGTTCCGGCGCGAGGACATCGGCTGGGAAGGGGCGCTTG
CCACCGTCGTGAAGACCCAGATTGAAGGTGTTCTGTCGTCTACGACATGACCCCGCGGACGAGAAGAACCTTG
ACCGGTGGGAAGGCTCCGAGTTCGGCATCCACCANAAGATCCGATGCCGCGTT (SEQ ID NO. 386)

Clone Rv308

.....Rv308SP6.seq:.....
CTCAAGCTTGATTTTTCATCATGATGATCATCACCCGAAGTGTGGTAGCCGCAGTGGTTATCGTGGGTACCGTCG
TGCTTTCCATGGGCGCCTCTTTCCGGCTTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGATGG
TGTTCGGCATGTTCGGTATCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAAANG
AAATTGGGGCCCGATTGAACACCCGAATTATCCGTGCCATGGCTGGTACCGGGGGAGTGGTGACGGCTGCCGGCATGG
TGTTCCGCGTTACCATGTCTGTTGTTGTGTTACGCGATTGCGAATTATTGGTCAGAT (SEQ ID NO. 387)

.....Rv308T7.seq:.....
CGNCCAAACCGAATTGGTTTTTCGGCGCCNTCCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGAC
ACACCTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCG
CCNCGGCGTTACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGC
CAAGGCGCGCTGCCAGGTGCCCCGGGCGCACGGTGCGGACAAGGTGGTGTGCGCGGTCCCGATCGGCCCANACGACAT
CGTGGCGAGATTGCGCCG (SEQ ID NO. 388)

Clone Rv309

.....Rv309SP6.seq:.....
CGTGAATGCCACCGGGGCCACTCCGCAGAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTCGCCGA
CTTTCGCGGTTACCCGCTCAACTTTGTGTGNACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTT
CATCTGACGCCGGAACAAATTGACNCAGCGGTTCCNCTGACCAATACGGTCGGTCCCACGATGACCCANTACTACNT
CATTCGCACGGANAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGAACCCACTGGCGAACCTGGT
TCAACCAACTTGAAGGTGATTGTTAACCTGGGG (SEQ ID NO. 389)

.....Rv309T7.seq:.....
TCGCTCAAGCGCNTGAGGCCGAANC GGCTGGTTACGACTCCCTGTTTGTGATGGACCACTTCTACCAACTGCCCATGT
TGGGGACGCCCGACAGCCGATGCTGGAGGCCTACACGGCCCTTGGTGCGCTGGCCACGGCGACCGAGCGGCTGCAAC
TGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCCTGCTGGCAAAGATCATCACCAGCTCGACGTGGTTA
GCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGTGCTGGAACACCGCCAGCTCGGCTTCGAGTTCGGCA
CTTTCAGTGACCGGTTCAACCGGCTCGAAAAGGCGCTACANAT (SEQ ID NO. 390)

Clone Rv30

.....Rv30SP6.seq:.....
ATACTCAAGCTTCCGCTGGGGCCTGTCAACCATGGCGATCCCGTTGGTCCCGGACATCCCGAACGAGGACACCCGGA
CCCNCTTCGGTGTGTGATCATTACCGTTGGGCCACTGCGTAACCGCTTGCGGCACAAAGAGCCCGGTCTCGACGTCCG
AAAGCTCATCGGGCACCCGATTGAAATGCAGCAGCGGCGGCCACCCCGTGCCGAGTGACAGAATTGCCTTGATCA
GCCCCGACGGTCCCCGCCGATGCCGTGCTGTGCCCCATGTTGCTCTTGCCGATCCAAAGCGCGCAGGGGGGTGCCGCGC
CATAACCCGCGCCAGGCTGCGGTACTCAATCGGGTCCGCCATTGGCGTACCGGTGCCGTGCGCCTCCACCACACCGA
CCGTTTCGGGCTG (SEQ ID NO. 391)

.....Rv30T7PEG.seq:.....
CAACAGCGTTCAGCGGCATACCACCGCACATGCCGTGCACCCGGCGCGGGCGGAGTCGCCGATAACACANGTACA
CCTTGGGAATCGGTGTGCGCCAGGGATTNACCGCGGGGTGGGGCCGGCGATCGCGCGCCAGGTGAGTTGGCGCCGA
CCGTGATNTCACCGCCGACGTAGTTGGCGTTGTGGTCCGCCATCCGCGCGGCGGGCACGGCGGGGCCGCCACACGA
TGTCACGGAAGCCGGGGGCGAACGCTCGACGACCTGGTTACCGTCTCNGTCGCNTCNANCGTGGACCCGACNGCACGT

GGGCATATGTCCANAACGGACGNGGCCGGTTTCNTCGATGCNGCCGGGGTCCGCGACNTGCGGACNCNCNGNCACACC
ATCCGCCAGTCCGCGTGGCGTCCCGCCGCGACTCTGCCTCGGCCGCGCCA (SEQ ID NO. 392)

Clone Rv310

.....Rv310SP6.seq:.....
CTCAAGCTTTGNCGACGATCGGGCGATGTCGATGANAGGAAACCCAGCGCACAACCGACNATTTTGGCGTAGCCGGC
GGACNTCTGCTCGATTCCGATCACGTCCGCGCTCGCATCGAGCATGGCGCCGGCGACGGCTAGCAGCGATCCGCCGTC
GTCGAGGAACACGACACGAGCCGTACGCCCGGCCGTAAGCCGCGCCAGGATTCGGCGAAAAACCGTTCTACGTGGCG
GGTGTACTGGGTGTCCAATGATTCGTGGGGTGCCTAGGCGTCTGCTGCAATCGTCGACATAAATGCCGTCCGCCCGCAT
CGCGTCAACAACCTCCCGGGTGAGTGGAATANCACTTGCCGA (SEQ ID NO. 393)

.....Rv310T7.seq:.....
TCCAACGCGGTGACAGATTTGTCTATCCTGGACCTGACGGTGAGGTGCAAGTTTCCAGGAATTCGGCAAAATCGGTA
AGAGCCTGAAGAATTCGGTATCGCCGGACGAAATCTGCGACGCATACGGGGCAGATACGCTTCGGGTTTACGAGATGT
CGATGGGGCCGCTGGAGGCTTCACGTCCATGGGCCACAAAGGATGTTGTCGGCGCTACCGTTTTCTGCAGCGGGTGT
GGCGCTTGGTCTGTCGACGAGCACACCGGCCGAAACTCGGGTGGCTGACGGCGTGGAACTCGACATCGATACGCTACGGG
CGTTCACCGCACCATCGTCGGCGTGTC (SEQ ID NO. 394)

Clone Rv311

.....Rv311SP6.seq:.....
CTCGTCCTTGACTACGCCAGTATCGAAANCCTCCTGTGCCGGTNCGCTAAACACCCGGCGGACACTCANACGGTGCT
GGTGGTGCGGCATGGCACCGCGGGCAGCAAAGCGCACTTCTCCGGGGACGACAGCAAGCGACCGCTAGACAAGAGGGG
TCGTGCGCAGGCAGAACGCTTGGTACCACAGCTGCTGGCGTTCCGGCGCCACCGATGTTTATGCCGCCGACCGGGTGCG
CTGCCACCANACNATGGAGCCACTCGCCGCGGAACTGAACGTGACCATAACAACGAGCCNCCTGACCGGAAGAGTC
CTACGCCAACAAACCCAAACGCGGCCGACACCGAGTGCTGCAGATCTTCG (SEQ ID NO. 395)

.....Rv311T7.seq:.....
GTATCGCCTCCNCCTTTGGCCACCAGCAGCCACAGCGCGGTTCCGGGACCGAACGTGGACATCAATAGCCCGGAATCG
GTGTGTGCAAGTTGGTAAACGGTGTTGATCCCAAGCTTTCGAGCCTTTTCGTAGTCTTGGGCCCCACACCCACAGT
GCTTCGACGGTACGGTCACCCATGATGGCCATCCAGTTGGCATCGGTGAGCTGATAGATGCCAGCTGGTTTCGCCAAC
CCGGTAGCGATCTTGGCGCGCTGCTTGTGTCCTGATACCTATCGAGCAAGACAGCCCGGTTTGGCACAAGATGACT
TTTCGGATCTCTTCNGCGAACTTCCAATGGGGTCTCCGGGANT (SEQ ID NO. 396)

Clone Rv312

.....Rv312SP6.seq:.....
CTCAAGCTTTTGGTCTAGCCGGCCGAGCAGATACGGGTGTCTTGGCCACCGCGCGCGCTGTCCGGGAAATGGCGG
GTCCCCGGTGGTTTTGCTGANGANTGCTGAACCGTAGTCGAAGTGGGCGGCGTCAGACTCCACCCAGCCAGCAGGCAG
CGCGAAGCTGAATCCTCAACCGGGTTGTCGATCCGGACAGGTTGGGGTGGCTTTGGGGCAATGACAGGTGGCGGCGG
TGCGTTCCGGTCCGGCGCGGAGGTGCTGCGTTGGGATCNCCTGGCTGGGCATTCCGCNTNTTGGCGGCGGCGCGGTG
TGGGGGGGCAACANGTGTCCCGGTGCGGGTGGCGCTGC (SEQ ID NO. 397)

.....Rv312T7.seq:.....
ATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCTCGCCGACTTTCGCGGTACCCGCTCAACTTTGTGT
CGACCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTTCATCCTGACGCCGGAACAAATTGACGCAG
CGGTTCCGCTGACCAATACGGTCGGTCCCACGATGACCCAGTACTACATCATTCGCACGGAGAACCTGCCGCTGCTAG
AGCCAATCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAATTTGAAGGTGATTGTTAACC
TGGGTACGGCGACCCGGCCTATGGTTATTTCGACCTCGCCGCC (SEQ ID NO. 398)

Clone Rv313

.....Rv313SP6.seq:.....
CTCAAGCTTGCAATCGGGTCCGGATGCCCATGGTTGGAANATGGTCGCCCTGGCGTCNAATACGCGCGAGCGCATGA
GCTACCCGGTTCCGGAACAACGTATCGAAAAACGTGCGCACTGCTGGCAGATGGTATCTCCGATGTGGTTGTAATTTGTA
TCCCAACTCTAACTGTGCTATCGGATCAGCGTGAATATCGANATATTGCGAATGCGATGACAGGCCGCCATTCCGGTTT
ATTCGCTTACGCTTCCCGGGTTCGATTCTGCTGATGCACTGCCGCAAAACGCGGATATGATTGTTGAAACCGTATCTA
ACGCAATTATTGATGTGGTAGGCGGCAGCTGCCGTTTTGTGCTGTCGG (SEQ ID NO. 399)

.....Rv313T7.seq:.....

CAAATACACGCCGGACGCACAGGCGGACATCGCCATCCCGAGCACACCCAAAACGGGATACAGGATGGAGGCCAACGC
CACGGCCCGCGCCAGGATACCAACCACACCGGCTTGGTCAGCTTGTGGCGGGCGGTATAGGCATCGGGCCGCTGCAA
CGCAGCATGCACAAACCGGTACACCGCTGTACCAAGACGGCGACCAGCAATACCAGCATGACGGTACCCACGAGGTG
GCTCACGCATTGAGACTATGCGGTTTGCATCCAACACG (SEQ ID NO. 400)

Clone Rv314

.....Rv314SP6.seq:.....

CTCGTCCTTCGGCCTCGCTGCAGGAGTGGGAGCCGACGGGCTGGAAATCCGAAAAACGAGCCGGTGATCGCACTGTCTG
CCGATCGGGCGCCGACCTGGTTGGTGTACGGATGAATCCGCAGCGAAATGTGGCTGCGGTGGCGTGTCTGACTCGT
TGGCGTCGACGCTGGTGGCAGCCACCGAGCGGTTGGTCCAGGATCTGGATGGGCAAAGTTGTGCGGCCCGGCCGGTGA
CGGCCGATGAGCTGACCGAGGTCGACAGCGCCGTGTTGGCTGACTTGAACCGACATGGAGTCGCCCCGGTT

(SEQ ID NO. 401)

.....Rv314T7.seq:.....

GTCTAGNCCGCCGAACACGATACGGGTGTCTTGGCCACCGGCGCGGCTGTCCGGGAAATGGCGGGTCCCCGGTGGT
TTTGCTGAAGANTGCTGAACCGTAGTCAAGTGGGCGGCGTCAGACTCCACCCAGCCAGCAGGCAGCGCGAAGCTGAA
TCCTCAACCGGGTTGTGATCCGGACAGGTTGGGGTGCCTTTGGGGCAATGACAGGTGGCGGCGGTGCGTTCCGGTC
GGCCGGCGGAAGTGTGCTGCGTTGGGATCGCCCGGCTGGGCATTGCGCGTGTGGCGGCGCGGTGG

(SEQ ID NO. 402)

Clone Rv315

.....Rv315SP6.seq:.....

ACTCAAGCTTGAGATTGGCGTCAACGGGTGTGCGCACCGGCGTCTGCAAGTGGTAGGCCTGCAGTTTGTGCATCAGG
CCGATGCCGCGGCCCTCGTGGCCACGCATGTACANACCACGCCGCGCCCTCACGGGCGACCATCGCCAGCGCGGCG
TCCAGCTGAGGCCCCGAATCGCAGCGGCGTGACCCAAACACATCGCCGGTCAAGCACTCCGAATGCACCCGGACACG
ACGTCG

TCACCGTCGGCGTTGGGCCCCGGCGATCTCGCCGCGGACCAGCGCGACATGTTCCACGTCCTCGTAAATGCTGGTGTAN
CCGATGGCGCGAAACTCCCCATGACAANTCGGAATCCGCGCCTCGGCGACCCGCTCAATGTTGCTTCTCNTGCTTG

(SEQ ID NO. 403)

.....Rv315T7.seq:.....

TCGACNAGCATTCTTGACNGTTGTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCACCAGATCATCTTGGTC
CGGTAGCGCTCGTCCGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACGCCACCGGTCCAGC
GCGTGGGCGCGCGGTCCTCCATCACAACCTGAACCCCCAACAGGGGACATGCTTAGCGGTAGGGCGCGCGCCAAGGC
GGCAGCAATCGCATCACTGCGCTGCGCGTCACTATTAACCCACCCGGACTTCACTTCCACGACCCCGAATGGCGCCCC
GTCATTGATCATCTTGCGCACCGCGGATAATCCGGGAT

TG (SEQ ID NO. 404)

Clone Rv316

.....Rv316SP6.seq:.....

ACCGGGGCCACTCCGCACAATCTGTACCCGACCAANATCTACACCATCGAATACGACGGCGTCGCCGACTTTCCGCGG
TACCCGCTCAACTTTGTGTGNACCCTCAACGCCATTGCCGGCAGCTACTACGTGCACTCCAATACTTTCATCTGACG
CCGGAACAAATTGACGCGGCGGTTCCGCTGACCAATACGGTCGGTCCACNATGACCCANTACTACATCATTGCGACG
GANAACCTGCCGCTGCTAAAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAC
TTGAAGGTNATTGTTNACCTGGGCTACGGCGANCCGGCCTNTGGTTATTCCACCTCNCCGCCCAATGTTTGCNACTCC
CGTTCGGGGTTGTTCCCNNAAGGTCAACCC (SEQ ID NO. 405)

.....Rv316T7.seq:.....

CGCTCAAGCGCNTGAGGCCGAANCGGCTGGTTACGACTCCCTGTTTGTGATGGACCACTTCTACCAACTGCCCATGTT
GGGAGCGCCCGACCGGATGCTGGAGCCCTACACGGCCCTTGGTGGCGCTGGCCACGGCGAGCGGCTGCAACT
GGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCTGCTGGCAAAGATCATACCACGCTGACGTGGTTAG
CGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGANCTGGAAACACCGCCAGCTCGGCTTCGAGTTCGGCAC
TTTCAGTGACCGGTTT (SEQ ID NO. 406)

Clone Rv317

.....Rv317SP6.seq:.....

CTCAAGCTTGCGTTTCGATGAAGTAGTCTCGGTACGCGCCGCTCTTCGAGCTCCTTGGCGATGCCAGCAAGGAGTC
ATCGCCGCCGAGCTTGGCCAGGATCTTGTGCGGCTGTTCTTGACGATGCGGGCCCGCGGATCGTAGTTCTTGAGAC
ACGATGACCGAAACCATCAATTGACCCCGGCTCGCGGTTCTTGACCTGCGTACAACTCGCTGACGTGCTCGCC

GCTGTGCGGAATGCCCTCGAGCATCTCCAGGACAGCCTGATTGGCGCCGCCATGAAGCGGACCCCATAGTGCGTTGAT
GCC (SEQ ID NO. 407)

.....Rv317T7.seq:.....
GGTCAGGCCGAGCAGGCGCGAGGAACGACGAACCAACAAGCCATGGTGGTTGGCGCCGTCGAGAGGTGCGCGGTGCGC
CACAACGGGAAGATCGCCTTGAGCGTCGCTCGACCGCCGCTCGAGTTGGGTCATAACGAAGTAGCTGATGCCGATCA
TGTCGACGTTTCCGTCGCATCAGCGTGCAGCGGCGACCCACTCNACGAGGTCTCGGTGCCGCGCGGCCAGGGCACCA
GCAGTGACGAGTCCAGGCGCCGTCGGGCCAAGCAGTCGCGGTGCCANCCGTGGTGGTGGGCGGATGGTTGGGTGTGC
TCATTTGCGGAACGCCA (SEQ ID NO. 408)

Clone Rv318

.....Rv318SP6.seq:.....
TTCGAAGCTTTAACAGCATCAACCCCGCCCGCACCAGCACCAGACACNATGTCGATGCCATCGAGGTGAATGTCGAAC
ATGCGCAAACCATCGGCGACCGCGACCAACCGCAACATGGGTACCGGCGATTTCGGGTGCCAATGCCGACCCGACGGG
CCGCTCTCACCGCAGGTGACCTCGATCACCGAGACCANCCGGCGTTNTNNTCACGCACCCCTACCGTGTACGCCCCA
AAACGGGCGCTGGTGGTGCATTGCCGGAGTGACCCCNACCCAGTGTGTCGCCGCGATCC (SEQ ID NO. 409)

.....Rv318T7.seq:.....
TGATGCCGCACCCGATCGACGGTCTGTGGTGGGGTTGACTGGCCGCCCGGCGAAGCAGGGCGTCGACCGCGGCCCCG
ACGTGCGCGGCGCTCACCGGTGCGCCATTGCCCGGGCGGGAGTCGTGAGCTGACCACGGTAGACAAGTCGGCGCTGG
CCGTCGAAGACNAACGTGTGCGGTGTGCAGGCCGCGGAGAAGGCGCGGGCGACNTCTTGGGTTTCGTGCTANAGATAC
GGGAACGTCCAGCCGTGGCGGGGCGCTCGGCGACCATCTGATCGGGCCCGTCC (SEQ ID NO. 410)

Clone Rv319

.....Rv319SP6.seq:.....
TTTCGGGCGAGGCGGTATANCTTCCNCTCGTACCGGCGACCGCCAGCCGANAAGCTCGTTTCCAGTGTTGCTGGGG
ATTCTCACGCTGCTGCTGANTGCGTGCCAAACCGCTTCCGCTTCGGGTTACAACGAGCCGCGGGGCTACNATCGTGCG
ACGCTGAAGTTGGTGTCTCCATGGACTTGGGGATGTGCCTGAACCGGTTACCTACNACTCCAAGCTGGCGCCGTCT
CGTCCGCGAGGTGCTTGTGCGATAGCCGGGAGGCCCGGATCCGCAATGACGGATTCCNTGCCANCGCTCCGAGTTGC
NTGCGGATCGACTACNAATTGATCACCCANAACCATCGGGCGTNTTACTGCCTGAAGTACCTGGTGCGGGTCCGATAC
TGCTATCCGGCGGTGACAACCCCGCAAGC (SEQ ID NO. 411)

.....Rv319T7.seq:.....
GTTTGGCTCGGCATGGTTAGCCAAGTTCTGCGGTCCCACAGATCATCTTGGTCCGGTAGCGCTCGTCCGGGTATG
CTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGAACGCCACCGGTCCAGCGCGTGGGCCCGCGGTCCCCA
TCACAACTGAACCCCAACAGGGACATGCTTAGCGGTAGGGCGCGGCCAAGGCGGCAGCAATCGCATCACTGCGCT
GCGCGTCACTATTAACCCACCCGACTTCACTTCCACGACCCCGAATGGCGCCCGGTCACTGATCATCTTGCGCACCG
CGGATAATCCGGGATTGCCAGCCCATTCNACTACCGCATGCGAGTCATCGGCTGACCGCAGCGGTC
(SEQ ID NO. 412)

Clone Rv31

.....Rv31SP6.seq:.....
TCGCCTAGGCGGGCTTCCCTTCCGTCCGAGCNGTCAGAAGCTCCTATGACAATGCACTACCCGAGACNATCAACGGC
CTATGCAATACCNAGCTGATCAAACCCGGCAAGCCCTGGCGGTCCATCGAGGATGTCGAGTTGGCCACCGCGCGCTGG
GTCGACTGGTTCAACCATCGCCGCTCTACCGGTACTGCGGCGACATCCCGCGGTCTAACTCGACGCCGCGCTCACTA
CGCTCAACGCCAGAGACCANCCGCGGCTGACGTCTCAGATCAGAGAGTCTCCGGAATCACCGGGGCGGTTCTATCCCC
ACTGTCGATAGCGTCTGTGGATAACTTTGTCTGCA (SEQ ID NO. 413)

.....Rv31T7.seq:.....
GCGCGTNGAACTGATAGGTGCGGCGCGGCTCGAGCANGCCGGCCATTTGTTGATGCGGTTACCGAAGATCTCTTCGG
TGACCTGCCCGCGCGCGGCGAGCTCGGCCAGTGCCCGCGTGGCCGCCGCGGCGACAATCTTGGCGTCCACGGTGG
TCTGGGTCA (SEQ ID NO. 414)

Clone Rv321

.....Rv321SP6.seq:.....
CTCAAGCTTCAATACAGAGTTATAAACTGTGATAATCAACCTCATCAATGATGACNAACTAACCCCGATATCAGGT
CACATGACGAAGGGAAAGAGAAGGAAATCAACTGTGACAACTGCCCTCAAATTTGGCTTCTTAAAAATTACAGTTC
AAAAAGTATGAGAAAATCCATGCAGGCTGAAGGAAACAGCAATAACTGTGACAAATTACCCTCAGTAGGTGAGAACA

ATGTGACGAACCACCCTCAAATCTGTGACAGATAACCCTCAGACTATCCTGTCGTCATGGAAGTGATATCGCGGAAGG
AAAAT (SEQ ID NO. 415)

Clone Rv322

.....Rv322SP6.seq.....
CTCAAGCTTCGATCGACATTACTCCCGCCTTGGGTCTGGTCTCCGAGCTGGTCGGTCATGGTCGGACCTGCTGGTAGT
GGGGATCTAACGCAACATGGTCGGGATTCATCATGGTGATACCCGTCGACCTGCGAGCTGCCGGTGAAACCCCGC
GATGCCGGGATTTCAGCCGCACTAGGATGTCTAGCCGGCCAGCCGCTGCCGCCGGAATTCGGGATGTTCCGGTATACC
ANCGATCGGCAATCTTGCATATCCGCCGATGCTCGAACGCTANCCACGCCAAACCAACCACTGTGACNACAATCGCCA
CCACACCAAAGTCATGCCCTCGGCGTGATGTCGGTGCCGAAAGCCGCAAGAGCTCCGACGCCGCC

(SEQ ID NO. 416)

.....Rv322T7.seq.....
CATTCCCAATTGAATTTCCCNATCCCACAATCTCGGTTTCAGATACAGGTCGCCATACCCCTTACTTCGGCAACGCTGG
GCGGATTGGCCCTGCCGCTGCAGCANACCATCGACGCCATCGAATTGCCGGCAATCTCGTTTCAGCCAATCCATACCCA
TCGACATTCCGCCGATCGACATCCCGGCTCCACTATCAACGGAATTTTCGATGTCGGAGGTCGTGCCGATCGATGTGT
CCGTTCGACATTCCGGCGGTACCATCACCGGCACAGGATCGACCCGATTCCGCTGAACTTCGACGTTCTCAGCAGCG
CCGGACCCATCAACATCTCGATCATCGACATTCCGGCGCTGCCGGGCTTTGGCAACTCGACCGAGCTGCCGTCTCGG
GCTTCTTCAACACCGCGCGCGGTGGCGGCT (SEQ ID NO. 417)

Clone Rv327

.....Rv327SP6.seq.....
CTCAAGCTTTTCGGCGGAGACGGACANNTTGCGAACATTGATGACAAAATAGAAATCATTGATGGTTTGAGTCACCAGG
CCGATCAAGCCTTCGCCGAGCCAAATTCCAATCAAGAGGCCCAAGCCCGTACCAATCAGCCCGGCAACGAGGGATTCC
GTCATTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAATATGGCGAAAACGGTCGCCGTTGCACG
ACATTAAATGTCACGGTATTG (SEQ ID NO. 418)

.....Rv327T7.seq.....
AGCTTAACTGCTCCCTAATACCTGGGGCTGTGCTGCGGTGTATGCACGGCATAACGGACATCCNTCCCCTGAGACCCN
CGGTCTAATCAGCCACGTGTCCACCATCAGGGGTCAACCCCGGCCAAGGGCGACGGCACCCCAAGTTCCCGACCGTT
AACCTATTGCTGTGAGCTTCATTTGCTGCGAGCAAAACAGTTGGTCGGCCGTTAGGAACTGAATTGACACTCAACCGA
TTTGGTGCCNCCGTAGGTGTCTGGCTGCGGGTGCGCTGGTGTTGTCCGCTGTGGTAACGACCACAATGTGACCGGG
GGAGGTGCAACCACTGGCCACGCGTCCGCGAATGTCTATTGCGGGG (SEQ ID NO. 419)

Clone Rv328

.....Rv328SP6.seq.....
CTCAAGCTTGGGGTGGCGCTGTGCGTCGGTGTGCTTGGCGGCGTCGGTATCAACACCGCCACGAAATGGGGCACAAG
AAGGATTTCGCTGGAGCGGTGGCTGTCCAAAATACCCCTCGCCAGACCTGCTACGGGCACTTCTACATCGAGCACAAC
CGTGGCCATCAGTCCGGGTGTCCACACCGGAGGACCCGGCGTCGGCGCGGTTCCGGCGAAACGTTGTGGGAGTTCTCTG
CCCCGAGTGTATCGGCGGCTTGCCTCGGCCGTTCAATTTGGAGGCCAACGGCTGCGTCGGCTCGGCGTCAGCCCC
CT (SEQ ID NO. 420)

.....Rv328T7.seq.....
GCACCAAGGCCCCACACGTACCCCTGTGACCTCCTGCGCCGACCCCGCCGAGGTCCTGGCCGTTACCACCTGAACGG
GCGAGCCGGGAGTCTGGTACGCATCGAACAAAGAGCAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTTCGATGACG
GGGTTCNATCCATTTCAGGTCCGTCGCCGCGTCGGTCGAGTGGCGGTTCACACTCCAGGTACTCGACCTCAGACGAGA
GGACTCGATCCCATCTAGGTGTGGACGAAACAGATCTTCTGTCCGA (SEQ ID NO. 421)

Clone Rv329

.....Rv329SP6.seq.....
TCGCCTCCGCATATGGGTTCGACGCCAAGCGGGTCCGGATTTCTGGGCTTCATCGCTCGCGCCGTTCGCGACAAACAGCG
CGGTTCGAACCGACACTCGTTGTGATGTCCCAGCTATACCTTCGGTACGCACCCAATCGACCCCTACNCGGCTATCTCA
GCCGCGATCTCCAGGCTCCGCCGAGCCAGGTGCATCCCGGTCCGGATCCCACTAACCCGGCACCATTTGGCGTCN

(SEQ ID NO. 422)

.....Rv329T7.seq.....
GTCCTCGAGTGCCGCGCTCGNCAACNCCAGCGCCCGCGGCCACTTGGATGCGACCCGTTTCAAGTCCCTTCATCAT
CTGCGAAAAGCCTTGACCCATGGCTCCGCCAGGATCGCCGAGACCGGCACCCGGAGGTTGTGCAACGACAGCTCGCA
GGATTTCGACGCCCTTGTAAACCAACTTCGGCAAGTCCCGCGACACCGTGAGTCCCGGCCCGGGTTCGACGAGCAGCAT
CGACATGCCTTGGTGCCGCGGTGTGGCGTTCGGGTTCGG (SEQ ID NO. 423)

Clone Rv32

.....Rv32SP6.seq:.....
GGCATACCAATGTGGACTTCTGCTCACCCACGATATCCGTGGTCTGATCCGCTGCTGCGGCGGGCTGCNACCTGCNTC
TCNCGCGGACCCGCTNACTACATGGCNCGCGCCGACGCATACGTGCGGCGGGGACCCACTCCNACTGGTCGACGGTGC
TGGCCGCGTGTCCGCANGTCCCNAAACCCGCGCCGACCGACGAAACCGGCGCCGCTCCGTTCTGGACCAACGCTCATGT
GCCGTGCGGGTCCATGCTCGACGCCATCGAGACCGTAACCGCGTCTCGAGCGGTTGCGCTCCGGCTTCCGTGACAT
CTTCGTGGTCTGCTGCGCGCGTCCGCGCGCGGATGGTTCGACCACAACGCCAACCTCGGCGGTGACATCACCGTC
CGCGCCACTCGACCTGGCGCGCGATCGCGGCC (SEQ ID NO. 424)

.....Rv32T7.seq:.....
GTGAGCAGACCTACGCCNCCTGGTTGCGCCAACCTCGGTACCGATCATGGCGCGCNGCCTGTCGTACCGGATACCCAGC
GAACAAGACAGCCCGGTCCGCGACAAGATGACTTTCCGATCTCTTCGGCGACTTCCATGGGGTCTGTCGGAGTCCCG
GGCGCCACCGGAGGTAACCCCTCGTCTCAGTCCCATACGCGACCGGGTATCCACGTGCGCGCAACAACGCCACCACTC
CCCAGACGCGCNCCTGTACGCGGTGGGTTCCACNGCAATAAGTGGCCTCANGGCATCGTCCGGCGGGGTCNCNAAC
GCA (SEQ ID NO. 425)

Clone Rv330

.....Rv330SP6.seq:.....
CTCAAGCTTGAGGTTAACTTTGAACGGATCGAGCTGGACGTTTCGAGACGGTGATCGGGCCGAACCTGAATTGTCCGGT
AATGCCCAACGCAAAAAGCAGGGTGGTGGCCGGGGCGGTGAAACCGGCGTTCGGCGGCACCGTCGAAATCTATGTGGAT
TGCCGGAATGGGGATGTCCGGCACGGCGAAACCGTAGTTTCGCTTGTCCCGTGAGGCCAGGTGGATGGGGGAAAGAT
CCTGGTGTCCGGGATAATAATGGGGCCGATGCCGCCGTTGAAGTCCACTGGATCGGGAATCCGGAATCTTGATCCG
ACGTTACGGCCGAACAGGCCCTC (SEQ ID NO. 426)

.....Rv330T7.seq:.....
CGGCGACGTGCGGATACGCCGAGCAGTTGGGAATCGCTCTGCAGCAAACCAATATTCTGCGCGACGTTTCGAGAGGACT
TTTTGAATGGACGGATCTACCTGCCGCGCGACGAGCTGGACCGATTAGGCGTACGCCTCCGCTGGACGACACCGGGG
CACTCGATGACCCCGACGGACGGCTCGCGGCNCTGCTGCGGTTTCAGTGCCGACCGCGCCGAGACTGGTNTTCGCTGG
GACTGCGGCTGATTCCACACCTCGACCGCCGACGCGTGCCTGCTGTGCGGCCATGTCTGGCATCTACCGCCGTCAGC
TCGCCTTGATCAGAGCATCGCCGGCGGTCT (SEQ ID NO. 427)

Clone Rv331

.....Rv331SP6.seq:.....
CTATAAAATACTCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGGGTTCGGGCGCCG
GGCCCGGGCCGCGCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCCGGNTGCGCTACGTCNAGCCATA
CCGGGCGGAGCTACATCGGCTCGGCCGCGCAGTGTTCGGGCCCTTTTCGAGGTCNAGGTCNATACCGATTTCGCGAT
CCGCAGCCGACCCCTGAACNACANAACCGTGCCCTACTATTGCTTGTGCGGGGGCCAAAAACAGCTTGGCATCCT
GGCCCNATTGGCCGGCGCGG (SEQ ID NO. 428)

.....Rv331T7.seq:.....
CTTCGGTTCGAGTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATCTTCCATAGCCCGCCACACCTTCAGTT
GCTCACCGGAATCCAACCGGTAGAAGGTTCGGCGAGCGCTCGGCATTGGTCATCGGGATATGCCGCTCGGGACGGTCAG
AGCCCTCGGGTCCGGCCAGCACTCCGCGAGGCTTCGTCGGGGTGGTTCGCGACGCGCATGGGCCACCATCGCATTACCA
GGTCTGCGGAATCNCCANCAGTANACNGTTCCTTCTCTAA (SEQ ID NO. 429)

Clone Rv333

.....Rv333SP6.seq:.....
CTGGCACCAAGCCCCACACGTCACCTCTGTGACCTCTGCGCCGACCCCGCCGAGGTCCTGGCCGTTACCAACCGAAC
GGCGGAGCCGGAGTCTGGTNCGCATCGAACAANAGCAAGGTGCATGGGCGGAGTTGTTCCGCCACTTCGTCGATGA
CGGGGTCNATCCATTCGAGGTCGCGCGCGTTCGAGTGGCGGTTCACACTCCAGGTACTCGACCTCACAGACNA
AAGGACTCNATCCCATCTAGGTGTGGACNAAACAGATCTTCTGTCCGACNACTACACCACCAACCGAGCCATCGCCGC
CGCCCGGATGCCAACTTCGACGCGCTACTGGCCCCGGCGGGGGCGCTCCCCGGTTGTCAACACTTGCCGTGTTTCT
TCACGCNCTGCCCCACATCCAACCCCAACG (SEQ ID NO. 430)

Clone Rv334

.....Rv334T7.seq:.....
GTTCTTGGGCCCATGCGGAGGTATCGCCGTTTCCACCACGCGGTTCGGGGTGGCGTTGCATTAGCTCACCGATGGTGCG
CTTGTGAGGCCCGCGGGATACCCCGAGTGCCGGTAAACCATCTTGTGCTGC (SEQ ID NO. 431)

Clone Rv335

.....Rv335SP6.seq.....
CAATACTCAAGCTTGGCGTGCCGTTCCAACCCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCA
ACNACNACGTCTCGCGGGACACACCTCGATGCTGCCGCCATGGACGCGGTGGAACGCAAGCAGCTGATCGAGCTAC
AACGCCGCGCGGAACGCTTCCGCCGCGGGCGTGACCGCATCCCCTTGACCGGGCGGATC (SEQ ID NO. 432)

.....Rv335T7.seq.....
CNTCATGATGATCATCACCCGAAGTGTGGTAGCCGACGTGGTTATCGTGGGTACCGTCGTGCTTTCCATGGGCGCCTC
TTTCGGGCTTTCCGTATTGGTCTGGCAGGACATTCTGGGTATCGAGTTGTACTGGATGGTGTGGCGATGTCGGTGAT
CCTGCTCCTGGCGGTGGGATCCGACTACAATCTGCTGCTGATTTCCCGGTTGAAAGAGGAAATTGGGGCCGGATTGAA
CACCGGAATTATCCGTGCCATGGCTGGTACCGGGGAGTGGTGACGGCTGCCGGCATGGTGTTCGCCGTTACCATGTC
GTTGTTTGTGTTACGCGATTGCGAATTATTGGTCAGATCGGTACCAC (SEQ ID NO. 433)

Clone Rv336

.....Rv336SP6.seq.....
ATACTCAAGCTTTTACGGTGATCGCNCATCACCTGGTTTCATGAAGTGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA
ACATGAGCCAGCCTCTCGTCGGCGGTTCGGGTGCAGGTGCTCGGGCAGCTCGGCCGCNACAGCCGCTGACCCTGAAAC
CAGCTTCCATATCCCGCGANNAACGACGCCAGTCCGCTACGTNACCCCTCCGCGACTGTCCATGGACAACAGCGCGTT
CTCCACCGACCGGGCCCGGTGTGGGGTNTT (SEQ ID NO. 434)

.....Rv336T7.seq.....
GCTGGTAGAGTCGCTGACCGGTGCAGTTTCGACAATGTGGTGCCGGTTCGGCGGTACGTGCCATCGAGACACTGGC
GCAGGCTATCGCACCCGTTATCGGCTACGAGCAAATCGCGGTATGCGTTCTTGAGCATGAGTCGGCGACCGTCGTCAT
GGTCGACACCCACGACGAAAGACGCAGATCGCCGTCAAGCATGTGTGCCGCGGATTATCAGGACTGACCTCCTGGCT
GACCGGCATGTTTGGTCGCGATGCCTGGCG (SEQ ID NO. 435)

Clone Rv337

.....Rv337SP6.seq.....
GCTTTCCGCCGATACCCGCCATGTCNCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGCGGGATCCCAAAG
TGGCGATGATCGGGCCGCTACGTCGTGGTGTACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTCGGTCCACGC
GGTGCGGCACATGGTGGACACCACCCGCCACCGCGGGGTGAAGGCCTATGTCACCGGTCCGGCANCATCAATGC
CGACCAGGCCGAGGCCGGANACAAAANTATCGTAAGGTCAACCGCATCACNAGCATGGTGATCGCAGCAATGTTGCT
AGTGATCTATCGCTCCGTAATTA (SEQ ID NO. 436)

.....Rv337T7.seq.....
CTTCCAACCCGAATTGGCTTTTCGGCGCCATCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGAC
ACACCTCGATGCTGCCGCCATGGACGCGGTGGAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCG
CCGCGGGCGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGC
CAAGGCGGCGTGCCANGTCGCCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCCA
(SEQ ID NO. 437)

Clone Rv338

.....Rv338SP6.seq.....
TACTCAAGCTTCGCGAGATCCGGATGGCACTCACGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACT
TGAACCTGGTCTCGTTCCGCAATAACTCGTTCCGGCTGCAGGACGCGGCGAAACGTNCTTCGGCATCAACGCGTCCG
ANCTGAATTGGCAGCAAGCGGCGCTGCTGGCCGGCATGGTGCAATCNACCAGCAGCTCAACCCGTA
(SEQ ID NO. 438)

.....Rv338T7.seq.....
CCCACGACTTTCTCCTCGATCAGTTGGATTTGTACGAAGAGGCAACGAAAGCAGTGATCCTCGGGATGGTCGACGCC
ACATCGACCCGCGGTTACGCCGCACAGCCTGCTAGATGCGCTGGGCGAGCAGGTCCCACAGTTCCGCCGCTAAGGCAC
GGCGTCTGTTCCCGTCCGGATCGCCATTCCGGCTCGCGTCTGCTCCCATTCGATCAATAGGGCTGGCAGCTCCGTC
GGCAGGGGCTACGCCTCACCCGTCACG (SEQ ID NO. 439)

Clone Rv339

.....Rv339SP6.seq.....
CTCAAGCTTATGCGCGCGGCGGAGGTCTGCTCACGGCAACCCCTGAAGTTTAGGGGACNACCTACTCAGCGCAAAAT
TTCGCTAATGTGAGTCCGCCCCACAGGGGNANATCAACCATGTCGATCATGATCTACCCGGATACCGGATTGGCGG
TAGCGCCACGATCGTCNAAATNTCCGCCTGAATCATCGGATAGCTGATCCGGCGTCAACGCGTTTTGANTTCACCG
GCAACAGCCGCCAGGCCGGCCCGCANCGANCCGATCTCNTCGGGCCGCGATGGGCCCCAATCTTNTCG
(SEQ ID NO. 440)

.....Rv339T7.seq:.....
GTGTGTGGTGGAAACCATCTGAGCAGTGTGCCAAACCGGGGAGACAGCTCCCAATTGACGTGAGCCCGCTCACTTGC
TGGGTAAGCGTC (SEQ ID NO. 441)

Clone Rv33

.....Rv33SP6.seq:.....
CTTTACACTTCCTGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATG
ACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGGGCGTGACGGCCACCGGGGCACTCCG
CACCATCTGTACCCGACCAAGATCTAC (SEQ ID NO. 442)

.....Rv33T7.seq:.....
CAGGCATGCAAGCTTTAGCTGCCCGAATGCGTCACCCCGATGCGCCAGATCGGGGCTTCGCAGATAAAGCACGAACA
GGCGGGCAAAACGTCNATCTCGGAGCCGGAAGGGCAATCAGCCGACCGTCGACGAACGACACCGGGCGAGACCATTAG
GCAGTGACGGCCGGCCCGAACATTACGCGCTCGTTGATTAGGCGTTTCGGTCTCGTCCGCGGTCATGCCGAGCAGCTTG
CGGCAGATCTGAACGCTGCTCTGTCGGGCGAGCGGCGCGGGCGTTGGGGTGCTGCCCGAATGTGACGAAACGGAGC
CGGACCCGCTCTCGGCGGGCCGCGGACGGCGATCCGC (SEQ ID NO. 443)

Clone Rv340

.....Rv340SP6.seq:.....
CNCAAGCTTGCGGATGTTACCCCTGACAGCCTGAACATATGTNAAACACACGGCACCGGAACGGTGTGGGGGACCCC
ATCGANTTCGAGTCGCTGGCGGCCACTTATGGCCTGGGTAAAGGCCAGGGCNANAGCCCGTGCGCATTGGGGTCGGTC
AAAACCAACATCGGCCACCTGGAGGCGGGCGCCGCTGTGGCTGGATNCATCAAGGCGGTGCTGGCGGTGCAACGTGGG
CACATTCCCCGCAACTTGCACTTACCCGGTGAACCCGGCCATCNACGCGTCGGCNACGGGCTGTTCTGTCGCNACC
NAAAACCCCCCGTGGCCGGCGGC (SEQ ID NO. 444)

.....Rv340T7.seq:.....
GGAACCGGTAACCAGATCAGCTCGTCGACCTCACTGCCGGGGGTGAATCCCCACCGGTGCTGCGCGCTGCCAGTAG
TGCACCTTCTTGACGCCCTCGAAAAGGGGAGTCGGTCGGGTAGGTACCCGTCAGGAGCCGCCTACCCAGGTTGGCGCNA
TAGCCGGTCTCCTCGAGTATCTCCGACCCGCCCCACCGGTGCGGTCTACCCANATCCACTTGGCCCTTGGGCGAGC
GACCAGTCGTCTANCGGGGCGGTGAATGACAACGATCTCGACCGGCCCTTCN (SEQ ID NO. 445)

Clone Rv341

.....Rv341SP6.seq:.....
TACTCAAGCTTCAGAACAGGCCTGTTGTGGGCNACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCCC
GCACCGCCGGCATCTCCCGTCACGCAGGGCCGCGGCCCGCGCCGAGCGACGGCGTGTTCGCGCAGTTGCGCGTCAA
TGATGCTGACCTGATCGGCCACCCGGGCGTTCTCGGCGTCGTGCGGTTCACTAATCGCGGTGCTCAGCAGCGTCTCGA
CAGCCACCAACCGAGTGCGGACCACTGC (SEQ ID NO. 446)

.....Rv341T7.seq:.....
TAATGTCTTGCCAACGTACCAACAATCGCGATGAATTCAATCATGCCGCCAGGGCGGGCAACCCAATGGTGCGCGC
AGCGGCAGCTCGATCGCAGCGCGGAGGTTGCCGGCCGCGAGTTGATTACGAACAGGGTGAGGTCATAGGCGGGCAGG
ATAGTGACGAAGGCAAGACCTATATCTGCCGTGGAAGAAGAATCGAGTAGCCGGTCGACACAACGGAAGCGAAAGTG
TCCGCGATGTTGATGAGCGTCGCCGTTGTGGCGGCGGTGGCGGC (SEQ ID NO. 447)

Clone Rv343

.....Rv343SP6.seq:.....
TACTCAAGCTTTCGTGAGTTTCATCGCGCCAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAA
CGGTGATTTCTTGCCCGCCGCTGACGGCGCGAACGACGCCAGCGACCATTCAGCANATGGCCAGCGCGTGCCGGGC
CACGAGGTTGGTGCTCGGCGGCTACTCCAGGGTGCGGCGGTGATCGACATCGTCACCGCCGACCACTGCCCGGCT
CGGGTTCACGCAGCCGTTGCCGCCCGCAGCGGANNATCACATCGCCGCGATCGCCCTGTTT (SEQ ID NO. 448)

.....Rv343T7.seq:.....
CCACCCGTGTAATTTGGGATGGGCNAAAAGGCNAAAGCACCGGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGG
CTAGGGCTTCTCGCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGGTGCGCCCTCCGACCGCGAACATTCGGGG
ATGGCAGCAACCTGGTAGCACCTGGCCGGGCGATGATCTGCAGCGTCGCCGCGGGTAGTCGCCGCCCGGGCGGCTAC
AGTCTGAAACGCGATGACCATCGATGTGTGGATGCAGCATCCGACG (SEQ ID NO. 449)

Clone Rv344

:Rv344SP6.seq:::

450
TCAAGCTTTAGCTGCCCGAATCCGTACNCCCGATGCNCCAGATCGGGGCTTCGCANATAAAGCACNAACAGGCGGGC
AAAACGTCNATCTCGGAGCCGGAAGGGCAATCANCCGACCGTCNACAAACGACACCGGCGANACCACTTAGGCAGTGA
CGGCCGGCCCGAACATTACNCGCTCGTTGATTAGGCGTTCGGTCTCGTCCGCGGTATGCCGAGCAGCTTGGCGCANA
TCTGAACGCTGTCTGTCCGGGCAGCGGCCGGCGTTGGGGTGCCTGCGGAATGTGACNAAACGGAGCCGGACCCN
TCTCGGCG (SEQ ID NO. 450)

:Rv344T7.seq:::

CCGGGGCCACTCCGCACAATCNGTACCNNACCAANATCTACACCATCGAATACGACGGCGTCGCCGANTTTCGGCGGT
ACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAACTACTTCATCCTGACGC
CGGAACAAATNGACGCNTCGGTTCCGCTGACCAATACGGTCGGTCCC (SEQ ID NO. 451)

Clone Rv346

:Rv346SP6.seq:::

NCTGGCCTTTGGTCCACACTAANACAATACTCAAGCTTCCGGCCGAGAGCCGCCAACTCAGCATATCGTTAACCGAT
ATCCCGAGCCGATAGCTGGCGGGCTCGGGTGGTGGCCAGCGCGCTGCGACNAAAGGTGTGACCGTCATGAAACAGAC
ACCACCGGCGCGCTCGGCCGTCTGTCACCTGCTCGANATCTCAGCATCCGACGCCGGTGTGATCGCGCTTTCGGCGTG
TNGTGGGTCTCCGCCCGAGCCCGGCAAGGCCGGCCGACACAACCCCGGAAC (SEQ ID NO. 452)

:Rv346T7.seq:::

CATCTGCCACACACGACCGCGGTGCGGACGCGGCTGACGCGCTGGTGGTCTGAGCATCGTGGCCGGTCTGCTGTTG
TATGCCAGCTTCCCGCCGCGCAACTGTGGTGGGCGGCGGTGGTGGCGCTCGCATTCGTGGCCTGGGTGCTGACCCAC
CGCGCGACGACACCGGTGGGTGGGTGGGCTACGGCCTGCTATTCCGGCCTGGTGTCTACGTCTCGTTGTTGCCGTGG
ATCGGCGAGCTGGTGGGCCCCGGGCCCTGTTGGCACT (SEQ ID NO. 453)

Clone Rv347

:Rv347SP6.seq:::

GACAATACTCAAGCTTGACTGGCCACCCACCGGCATGACCACCGACAGGCCCGACTGGTTCGTACCACTCGAACGCCGG
GGTGTGATGTCCAGCCGCTGAANTCGTCTGCGCGCGCAGGCCGTGNAACAGGTACAGGGCGGGCGAATTGGCACC
ACCACTTTGGAATTGGACCTTGATGTACGGCCCATCGACGGCGACGGCACCTGCAGGTACTCCACCGGCAAGCCCGG
CCGGGAAAATGCCCCCGCGGTCTCCGTCACCGACCGCGCGGANCAAAACCCGACACTAGGGCCGCGCCNACGGCCCC
GACCACNANTCNACGCGACATACCCGTGACGGCGCCACNAACCTGTCAACA (SEQ ID NO. 454)

:Rv347T7.seq:::

CCTCCAACCTCGGCGGGGAAGCGACNCCAGCCTACCGAGCTTGGAGTCCANGACGCCAGCGGCGGCGTCTGGTCTGCGTC
GTGGTGCCCGCGGGGTGGCGTTGGCTGGCAACGATCTCCACCCAGCCGGTTCGGGTACCCACGATCTCGGCATANACG
CGGGCCGAGGCCGTCGATACCGTATTGCGTCAATTGGGACGCGGTTGTGCATTCCGGCTAGCTCGGTTGCCACACCC
GTCAGGGGTTTCGACGTTGGCGGGTTCGGCGGGCCCCANACCGCTGTACCATGCCCGCCAAGCCGACCTGCGGCGCC
ACCAACTGCAGCACCANCATGTGCGCGTCTGCGCGCCGCGATCACATGG (SEQ ID NO. 455)

Clone Rv348

:Rv348SP6.seq:::

CTCAAGCTTTTGTAGCGTCGCGCGGGGCANCTTCGCCGGCAATTCTACTANCGAGAANTCTGGCCCGATACGGATCTG
ACCGAANTCGTGCAGTGCANCCACCCTCATTGGCGATGGCGCCGACNATGGCGCTGGACCGATCTTGTGCCGCTT
GCCGACGCGGACGCGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCGACGCTGGTCCGCGTT
GCGCCGCNAAAGCGGCGGGTTCGGGTGCCATCAGGAATGCCTCNCCGCCGCGGCACTGCACGGCCAGTGCCGCGGCGA
(SEQ ID NO. 456)

:Rv348T7.seq:::

CNCCAGCTTGATTGGTCTGGTTGCATTGGCCAGCTGCGCGAGCCTGGCTCACTTCAACTACGACGACCGCAACAATT
GCCGCCTTCGGATCCGAGTTCCGTTGGGTACGCGGCAATGGAGCACCATTCTCGGTGAATCAGACTATTCTGAGTA
CTTGATCATCACTCTGCACACGACCTGCGAACCCGCGCGGCTTGCCGACCTGGAGCAGCTGGCGCAACGTGTGAG
CCAGATCCAGCGGTTGCCATGGTTCCGCGGTGTGACCCGGCCAAACGGGAAAC (SEQ ID NO. 457)

Clone Rv349

:Rv349SP6.seq:::

CAATACTCAAGCTTGACTGGGCCGCACTTCGGCGCCACCCACACCGTCAACGCCCGCGAAGTCNACGTCGTCCAGG
CCATCGGCGGCTCACGGATGGATTCCGGCGGGACGTGGTGTGACGCGCGTTCGGCCGACCGGAAACCTACCAGCAGG

CCTTCTACGCCCCGCGATCTCGCCGGAACCGTTGTGCTGGTGGGTGTTCCNACGCCCCGACATGCGCCTGGACATGCCGC
TGGTCNACTTCTTCTCTCACGG (SEQ ID NO. 458)

.....Rv349T7.seq:.....
TCGACGGTTTGGCGGCCTTAAATGCACTGAGGTCGTCAATTGACCCACAGCGGAAATGCCGACTATTGCGAGGCCCTC
CTTCGCCTTGGCTGCCGGAGAGGGGCTCCGCGGAACCGCATGCAGGTATATGACCTCGGTTTCTCGGGTGCTACCGC
GTGCCTTGTNTANGATNANCTCGGCGTTGGAATTGCCAGCCGGCCCAATTCATCGAGCGCANATTGCTACACNTGGC
CGGCGCGGACATACGCTTCACCGTGGATCTGCTCCACACGGAACCGCCCTGTCGGGATCCTGCTCACGGGTAANGGAAC
TTACGTGGCACTCGG (SEQ ID NO. 459)

Clone Rv34

.....Rv34SP6.seq:.....
GACCACGCCAGGCTAATCACGTGACGTACCGAATACCCTNCCTAGTGGTGCAGGCTCCCGCTGGAAATGGCCCTGTA
CCAACTCGCGCACCGGTGCCAG (SEQ ID NO. 460)

.....Rv34T7.seq:.....
CGGCACCCGACCCCTTTGAGCCGTCCGCCGTGGCCGCGGTGGAACCTGGCCGACGAGGGACTGATCGTGCTGGGCAAAT
TGGTCGATGGCACGCTGGCCGCCGATCTGAAGGTCN (SEQ ID NO. 461)

Clone Rv350

.....Rv350SP6.seq:.....
CTCAAGCTTGCCGTTACCCGACTTCCGGAGGGACACCATGAGCACCGCCAGCCGAGCACGAGGCCAACTCCGCCGA
CGCAGGCCGGTTGGACTTGCTGCTGGACAAGGGGTTAGCCGCCGAAGCAGTGACGTACATCGGCGAAAAGCAGTT
CGCCTGTCGACCGACGNGCANNACCGTGAGGCTAGGGAAGCGAGGAGCACATGGCCGCCGACCCGCAATGTACACGCT
GCAAGCAAACCATCGAACC CGGATGGCTATNCNTACCGCCCATCGCCGCGGT (SEQ ID NO. 462)

.....Rv350T7.seq:.....
CATGTCGCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGGCGGGATCCCAAAGTGCGGATGATCGGGCCGCC
TACGTCGTGGTGACCTCGTCGGTAACAACGAAACCGAAGCGTATGACTCGGTCCACGCGGTGCGGCACATGGTGGAC
ACCACACCGCCACCGCACGGGTGAAGGCCTATGTACCGGTCCGGCAGCACTCAATGCCGACCAGGCCGAGGCCGGA
GACAAAAGTATCGCTAAGGTCACCGCGATCACGAGCATGGTGATCGCAGCAATG (SEQ ID NO. 463)

Clone Rv351

.....Rv351SP6.seq:.....
ATACTCAAGCTTCGGTACGGTGGCGGGCCGTGCTGCTGGCCGCGGTGCGCGCGTGC CGGCCTGCGGTCTCGTTTACN
AGCTCGCGCTGCTGACACTGGCGGCNAGCCTGAACGGCGCGCGGATCGTGGCCACCTCCCTGATCGTCGCGGGCTACA
TAGCCGCGCTGGGAGCAGGCGCCTTGCTGATCAAGCCGCTACTTGACACGCGGCCATCGCGTTTATCGCCGTGGAGG
CGGTGCTGGGCATCATCGGC (SEQ ID NO. 464)

.....Rv351T7.seq:.....
TGTCAAGTCCTTTCAGATCTCNTTTTATGACATGACTGGAGATCTGTCTAGATTGCAGCTCCTGTGAGCGTGGGTAC
CGGATTCAAGCCGGTCGGTCACGCCGCGGTGGTACCGGCTTTCGCGCAGTGCTCGGCCTCGAGTTCGGCGATCGCGCG
CGAAGTGCGTTCGCGCAGCAAGATCGCGGCCGTAATGCGCGCGATGACCGCGATGACCAGCGCGATCCAGGAGAACCG
TTCCAACCAAGTGCTGGGCGGCCATCCCGCGAAGTAGACCAGTGCAAGTGGTGCC (SEQ ID NO. 465)

Clone Rv352

.....Rv352SP6.seq:.....
CAATACTCAAGCTTCAAAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAANTGCCG
CCCGCACCGCCGGCATCTCCCGGTACGCAGGGCCGCGGCCCGCGCCANCGACGGNGTGTTCGCGCAGTTCCGCCGT
CAATGATGCTGACCTGATCGGCCACCCGGCGGCTTCTCGGCGTCTCNCGTTCACTAATCGCGGTGCTC
(SEQ ID NO. 466)

.....Rv352T7.seq:.....
TACGCTGGCGCTGGAGGGAGCCANNTACAACATCCACGCCAATGCTCTTGCCCCGATCGCGGCGACCAAGGATGACCCA
GGACATCCTGCCGCCGAAGTACTGGAAAAGCTCACACCCGAGTTCGTGCGACCGGTGGTGGCCTACCTGTGCACCGA
GGAGTGTGCCGACAACGCATCGGTGTACGTCGTGCGTGGTGGCAAGGTGCAGCGAGTTGCGCTGTTTGGCAACGACGG
CGCAACTTCGACAAACCGCGTCCGTACAAGATGTTGCGGCGCGGTGGGCCGAGATCACCGATCTGTCCGGTGGCAA
AATTGCTG (SEQ ID NO. 467)

Clone Rv353

.....Rv353SP6.seq:.....
 GCTTTTCCCGTCCGTCNNCGCTCAACCGCGTGAGGCCGAAGCGGNTGGTTACGACTCCCTGTTTGTGATGGACCACTT
 CTACCAACTGCCCATGTTGGGGACNCCCGACCGCATGCTGGAGGCCTACACGGCCCTTGGTGCGCTGGCCACGGC
 GACCGANCGGTGTCNNNTGGGCGCGTTGGTGACCGGCAATACCTACCGCAGCCCGACCCCTGCTGGCAAANATCATCAC
 CACGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGCATTGGAGCCGGTTGGTTTGANCTGGAACA

(SEQ ID NO. 468)

.....Rv353T7.seq:.....

CNGCTTTTTAATGGCCTTGACNTGGGCGNGCCGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTAC
 ACCATCGAATACGACGGCGTCGCCGACTTTCCGCGGTACCCGCTCAACTTTGTGTCGACCCTCAACGCCATTGCCGGC
 ACCTACTACGTGCACTCCAATACTTCATCCTGACGCCGGAACAAATTGACGCAGCGGTTCCGCTGACCAATACGGTC
 GGTCCCACGATGACCCAGTACTACATCATTGCGACGGAGAACCTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATC
 GTGGGGAACCACTGGCGAACCTGTTCAACCAAACTTGAAGGTGATTGTTAACCTGGGCTACGGCGACCCGGCCTAT
 G (SEQ ID NO. 469)

Clone Rv354

.....Rv354SP6.seq:.....
 CTCAAGCTTGCCGGGAGGGTGTCATGGCCGACTCGGATTTACCCACCANGGGGCGCCAACGCGGTGTCCGCGCCGTCNA
 GCTGAACGTTGCTGCCCGCCTGGAGAACCTGGCGCTGCTGCGCACCCCTGGTCGGCGCCATCGGCACCTTCGAGGACCT
 GGATTTGACGCGCGTGGCCGACCTGAGGTTGGCGGTGGACGAGGTGTGCACCCGTTGATTGCTCGCTCGGCCCTGCCGGA
 TGCCACCCTGCGCCTGGTGGTCGATCCGCGAAANACGAANTTGTGGTGGAGGCTTCTGCTGCTGCGACACCCACNA
 CGTGGTGGCACCGGGCAGCTTTAGCTGGCAT (SEQ ID NO. 470)

.....Rv354T7.seq:.....

CCGACGCCGTCGTGGCCACCAACACCGCGACAGCACCGTGACCCGGACCGGGGTGCCGCGGAACCGGTCTTGGCCA
 ATTGCCCGCGCACCAGCCGTCGCGGCCATGGCGAACAGCACGCGGCATTGCCCGAGCATCAACACCATCACCAACCG
 TGGAAGCCCGGCCAGCGCGCCGACGAGATGATGCCGCTGGCCCGAGTACACCCCGTTGGCCTGGAACGCGGTGGCCA
 GATTTGCCGGCCCGCGGCCCGGTACGGTCCGCGAGTTGGGTGTATGGAACCATGCCCGACAGCACCAACCG

(SEQ ID NO. 471)

Clone Rv355

.....Rv355SP6.seq:.....
 TTNACTGGCCTTTGGTCCACACTAGACAATACTCAAGCTTCCAGGACATCGTCATCGCGACCAAAACCGCGAGCTAGG
 TCGGCATCCGGGAAGCATCGCGACACCGTGCGCGCCGAGCGCGCTGCCGGCAGGCCGATTAGGCGGGCAAATTAGCCC
 GCCGCGGCTCCCGCTCCGANTACGGCGCCCCGAATGGCGTCACCGGCTGGTAACACGCTTGCGCGCCTGGCGGGC
 GCCTGCCGATCAGGTGGTAAATGCCGACA (SEQ ID NO. 472)

.....Rv355T7.seq:.....

NGACGTCTTCCATCCGCGCGTCGTTTGGCGGGTTGGCCACAGCAGCCCGCCGGTGACGGCGACGATGCTGGGCTGGT
 TGCGGCCCTGCGCCACCGCGGCTTGATGCTGGTTGGCTGTCTGGGACGATCCCGAAATAGTCCACGCGGATCTGGT
 GATTTTGCGGCTACCCGCGATTACCCGCGCGGCTCGACGAGTTTTTGGCCTGGACTACCCGCTGGCCAATCTGCT
 GAACTCGCGGCCGGTGGTGGCCTGGAATGTCGAGCGCGGTACCTA (SEQ ID NO. 473)

Clone Rv356

.....Rv356SP6.seq:.....
 CTTCTCTCTGAGTACCNCCGNTACTTTGGGATGGGTAAGGCGAATCNCCGTTTGGTCACGAACGCCGGGAGGG
 ACAATCTCGGGCGGCTGGGGCCTCTCGCGGAANGCCCGAATGTACGGTGTCTCGACACTTCCNTCCCTCCG

(SEQ ID NO. 474)

.....Rv356T7.seq:.....

GAGCATCGGGACNTACGGAGTCACTACCCGCCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACGACGCCNG
 CGACCACATTGAGCAGATGGCCAGCGCGTGCCGGGCCACGAGGTTGGTGCTCGGCGGCTACTCCAGGGTGCGGCCNT
 GATCNACATCGTCACCGCCGACCACTGCCCGGCTCGGGTTCACGCAGCCGTTGCCGCCNCAGCGGACGATCACNT
 CGCCGCGATCGCC (SEQ ID NO. 475)

Clone Rv357

.....Rv357SP6.seq:.....
 TACTCATGANCATCCTTTAATCANNGCTTTGCGTTTTTTTTATTAAATCTTGCAATTTACTGCAAAGCAACAACAAAT
 CGCAAAGTCATCAAAAACCGCAAAGTTGTTTAAATAAGAGCANCACTACAAAAGGAGATAAGAAGAGCACATACCT

CAGTCACTTATTATCACTAGCGCTCGCCGCGAGCCGTGTAACCGAGCATAGCGAGCGAACTGGCGAGGAAGCAAAGAAG
AACTGTTCTGTGATAGCTCTTACGCNCA (SEQ ID NO. 476)

Clone Rv358

.....Rv358SP6.seq.....
CTCAAGCTTCAGGTCAATGTGCNCCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCGCCGGANACNCTGCCAAGGCC
ACCGAATACAACAACGCCCGGAGGCGTTCGCANCCAGCTGGTGACCGCCGAGCANANCGTCAAAAACCTCAAGACG
CTGCATGACCAGGCGCTTANCNCCGCANCTCAGGCCAAGAAGGCCGCTCNAACGAAATGCGATGGTGTGCACCANAAAG
ATCGCCGAGCGAACCAAGCTGCTCAGCCNG (SEQ ID NO. 477)

.....Rv358T7.seq.....
CATGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTGATGCCGACTCTGGTCAGCTCGGANCCGCTGACACCCCGCT
AAGGCTGCTCAGCTCGGTGCATTACCTCACCAGCGCGGAACTCCCCAGCTTTACGACTATCCGGATGACGGCACCTG
GTTGCGGGCGAACTTCATCATCAGCTTGGACGGCGGCGCTACCGTCGATGGCACCAGCGGGCGATGGCCGGGCGCGG
CGACCGATTCTGTTCAACCTGTTGCGTGAACCTTGCCGACGTGATCGTGGTGGCGTGGGCACCGTGCAGATTGAGGG
CTACTCCGGCGTCCGGATGGGTGTGCTCCAGCGCCAGCAC (SEQ ID NO. 478)

Clone Rv359

.....Rv359SP6.seq.....
TACTCAAGCTTGCGGGTGATCGCCTTGGTCAACGGCACCGTGATCGGATCGGGGTCNACCGCACAAATGGACTGGAGC
TTCGGCGAANTCATCGCTATGCCTCGCGGGGGGTGACGCTGACCCCGGGTGACNTGTTCCGGCTCGGGCACGGTGCCC
ACCTGCACGCTCGTCTATCACCTCNGGCCACCGGAATCATTCCCGGGCTGG (SEQ ID NO. 479)

.....Rv359T7.seq.....
GTTGGNGCCTCGTCGGCGAACAGTTCTCGCACGATTTCCGGATTAGCGGGACTGGTCACCAGTTGGGTATGCGGGAAG
GCGCTGACGTTTCGCCGCGATTAGCTGTTTGTGACGCGGTTGGTGATGTTCTGATCAGGAACTGGCTGTAATAGCCC
AGGGTCGCCACGCTTTTCATCCGGGCGCGGACCCGCGCACCGAGCGTGTGCGCGAGGTATGCGACGTGATTTTCGCTG
AAGTCCCCGTACCCGGAGAACT (SEQ ID NO. 480)

Clone Rv35

.....Rv35SP6.seq.....
TGCTTCCGGCTCGTATGTTGTGTGAATTGTGANCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTCCAGGTCAATGTGCGCCAAGCCCTGACGCTGGCCGACCAGG
CCACCGCCGCCGGAGACGCTGCCTTTGTACCGAATAACAACGCCGCCGAGGCGTTCGCAGCCCAGCTGGTGACCG
CCGAGCAGAGCGTCGAAGACCTCAAGACGCTGCATGACCAGGCGCTTAGCGCCGAGCTCAGGCCAAGAATGCCGTCG
AACGAAATGCGATGGTGCTCGGGCATAAGATCGCCGAGCGAACCAAGCTGCTCAGCCAGCTCGAGCAGGCGAAGATGC
ACGAGCA (SEQ ID NO. 481)

.....Rv35T7.seq.....
CAGGCATGCAAGCTTCGGAGGCAGACCCGTGCTGGTGCACTGTAGCGACGTGCTGCAATCAAGGTGATGCCCGACT
CTGGTCAGCTCGGAGCCGCTGACACCCCGCTAAGGCTGCTCAGCTCGGTGCATTACCTCACCAGCGGCGAACTCCCC
AGCTTTACGACTATCCGGATGACGGCACCTGGTTGCGGGCGAACTTCATCAGCAGCTTGGACGGCGGCGCTACCGTCG
ATGGCACCAGCGGGGCGATGGCCGGGCGCGGACCGATTGCTCTTCAACCTGTTGCGTGAACCTGCCGACGTGATCG
TGCTCGGCGTGGGCACCGTGCGCATTGAAGGCTACTCCGGCGTCCGGATGGGTGTCGTCATCGCCA
(SEQ ID NO. 482)

Clone Rv360

.....Rv360SP6.seq.....
TACTCAAGCTTGCGGTGGCGCTGTGCGTGGTGTGCTTGGCGGCGTGGTATCAACACCGCCACGAAATGGGGCACA
AGAAGGATTGCTGGAGCGGTGGCTGTCAAATACCCCTCGCCANACCTGCTACGGGCACTTCTACATCGAGCACA
ACCGTGGCCATCAGTCCGGGTGTCCACACCGGAGGACCCGGCGTGGCGCGGTTGGCNAACGTTGTGGGANTTCC
TGCCCCGCANTGTTATCGGCGGCTTGCCT (SEQ ID NO. 483)

.....Rv360T7.seq.....
GGCCATCGCCACCGCNCCGCGGCGAACGCTCAAAGGCACCTACTGGCACCAAGGCCCCACACGTACCCCTGTGACCTC
CTGCGCCGACCCCGCCGAGGTCCTGGCCGTTACCACCGAACGGGCGAGCCGGGAGTCTGGTACGCATCGAACAAGA
GCAAGGTGATGGGCGGAGTTGTTCCGCCACTTCTGTCGATGACGGGTCGATCCATTGAGGTCCGTCGCCGCTCGG
TCGAGTGGCGGTCACTCCANGTACTCGACCTCACAGACGAGAGGACTCGATCCCATCTAGGTGTGGACGAAACAGA
TCTTCTGTCCGACGACTACACCACCCAGGCCATCGC (SEQ ID NO. 484)

Clone Rv361

.....Rv361SP6.seq:.....
GCTTGC GG GTGATCGCCTTGGTCAACGGCACCGTGATCGGATCGGGGTCNACCGCNCAGATGGACTGGANCTTCGGCG
AANTCNTCGCCTATGCCTCGCGGGGGGTGACCCTGACCCCGGGTGACNTGTTTCGGCTCGGGCACGGTGCCACCTGCA
CGCTCGTCAAGCACCTCNGGCCACCGGAATCATTCCCGGGCTGGCTGCACNACGGCGACNTGGTCNCCCTCCAGGTG
AAGGGCTGGGCNAAACAANGCAGACCGTCCGGACAANCGGCACTCCTTTCCGTTGGCTCTTCGGCCGAATCCGGACG
CCNAACCCGACCGGCG (SEQ ID NO. 485)

.....Rv361T7.seq:.....
GTTCTCGCACGATTTCCGGATTAGCGGGACTGGTCACCACTTGGGTATGCGGGAAGGCGCTGACGTTCCGCCGATTA
GCTGTTTGTATGGACGCGGTGGTGATGTNCTGATCACGGAAGTGGCTGTAATANCCAGGGTCGCCNCGCTTTCATCCG
GGCCCGGACCCGGCGCACCGAGCGTGTGCGCGAGGTATGCGACGTGATTTTCGCTGAAGTCCCGGTACCCGGAGAACT
CGAACACGCTGAGGCGCTCGTCACCGTCGTNNCGGCGACCAAGCGCGGCGAGCAACTGCGCAAAATCGTTAAGANAGG
TCGAATCGTTGAAATTCGGCACCACTGCACC (SEQ ID NO. 486)

Clone Rv363

.....Rv363SP6.seq:.....
CACAAGACAATACTCAAGCTTCAGGTCAATGTGCNCCAAGCCCTGACGCTGGCCGACCAGGCCACCGCCGCCGGANAC
GCTGCCAAGGCCACCGAATACAACAACGCCGCCGAGGCGTTTCGACGCCAGCTGGTGACCGCCGAGCANANCGTCNAA
AACCTCAAGACGCTGCATGACCAGGCGCTTANCGCCNACGCTCAGGCCAAGAAGGCCGTGCAACGAAATGCGATGGTG
CTGCAGCANANATCGCCGANCAACCAAGCTGCTCAGCCAGCTCGAGCAG (SEQ ID NO. 487)

.....Rv363T7.seq:.....
CCACCCGTGCTAGGTGGCACTGTAGCGACGTGCTGCAATCAAGGTCATGCCCGACTCTGGTCAGCTCGGAGCCGCTGA
CACCCCGCTAAGGCTGCTCAGCTCGGTGCATTACCTCACCGACGGCGAACTCCCCAGCTTTACGACTATCCGGATGA
CGGCACCTGGTTGCGGGCGAACTTCATCAGCAGCTTGGACGGCGGCGCTACCGTCGATGGCACCAGCGGGGCGATGGC
CGGGCCCGGCGACCGATTCTTCAACCTGTTGCGTGAACCTGCC (SEQ ID NO. 488)

Clone Rv364

.....Rv364SP6.seq:.....
GCTTTCCGCCGATACCCNCCATGTCCCGCACATCCAGGACTTCTGGGGGGATCCGCTGACAGCGGGCGGATCCCAAAG
TGCGGATGATCGGGCCGCTACGTCTGGTGTACCTCGNCGGTAACAACGAAACCGAANCATGACTCNGTCCACGC
GGTG (SEQ ID NO. 489)

.....Rv364T7.seq:.....
CAACCCGANTTGGCTTTTCGGCGCCNTCGGTGAGGACGGCGTGCGGGTGCTCAACGACGACGTCGTCCGCGGGACACAC
CTCGATGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGATCTACNACGCCGNGNGGAACGCTTCNGCCGC
GGGCGTGACCGCNTCCCGTT (SEQ ID NO. 490)

Clone Rv365

.....Rv365SP6.seq:.....
GGGATGGGCAAAAAGGCGAAGCACCGCTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTCGCG
GGAAGGCCCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAATTCGGGGATGGCAGCAACCTGG
TAGCACCTTGCCGGGCGATGATCTGCCAGCGTCCCCGCGGGTAGTCGCCGCCCGGGCGG (SEQ ID NO. 491)

.....Rv365T7.seq:.....
CAGCAGACCAACAAGAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGGTGATTTCTTGCCCGCCGCTGACGGC
GCGAAGCAGCGCCAGCCACATTACGAGATGGCCAGCGCGTGCCGGGCCACGAGGTTGGTGCTCGGCGGCTACTCC
CACGGTT (SEQ ID NO. 492)

Clone Rv366

.....Rv366SP6.seq:.....
CTCAAGCTTGACTGGCCACCCACCGCATGACCACCGACAGGCCCGACTGGTCGTACCACTCGAACGCCGGGGTGTTT
GA (SEQ ID NO. 493)

.....Rv366T7.seq:.....
TTGGTGCCCGGAATGGCGAGTCCCATTTANTCGCTGATTTGTTTGAACAGCGACGAAACCGGTGTTGAAAATGTCGCC
TGGGTGCGGGATTCCCTCTCCAAGCAAGAGTAAC TGGCCCCAAATAAAGTTACTCGTCGTCTTGCAAAGACCGCTACC

CGATGCCATTATGTGTTTCCTTACGCTCANNNTCCGGTGCGCCATCATTATCTGCACCTTTGCACTGCACATTGAG
CTTAGCAGCGCTCG (SEQ ID NO. 494)

Clone Rv367

.....Rv367T7.seq:.....
GAATTNGCTTTCGGCGCCATCGGCCAGGACCGGTGCGGGTGCTCAACGACGACGTCGTCGCGGGACACACCTCGA
TGCTGCCGCCATGGACGCGGTGCAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCCGCGGGCG
TGACCGCATCCCGTTGACCGGGCGGATCGCNGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGCCAAGGCGGC
GTGCCAGGTGCGCCGGGCGCACGGTGCGGACAAGGTGGTGCTGGCGGTCCCGATCGGCCAGACGACATCGTGCGGAG
ATTCGCCGGGTACGCCGATGAAGTGGTGT (SEQ ID NO. 495)

Clone Rv368

.....Rv368SP6.seq:.....
TAAAGCTTTCGTCACTTCATNGNGCCCCGGACCAACAAAAGCATCGGGACATACGGAGTCAACTACCCGGCCAACGG
TGATTTCTTGGCGCGCGTACGGCGCNAACGACGCCAGCGACCACATTACGAGATGGCCAGCGCGTGCCGGGGCCAC
GAGGTTGGTGCTCGGCGGCTACTCCCAGGTGCGGGCGTGATCNACATCGTCACCGCCGACCACTGCCGGGCTCGG
GTTACGCGAGCCGTTGCCGCCCGCAGCGGACGATCACNTCGCCGCGATCGCCCTGTTGCGGAATCCCTCGGGCCGCGC
TGCGGGGCTGATGAGCGCCCTGACCCCTCAATTCCGGGTCCAANACCATCNACCTCTGCAACAACGGCGACCCGATTTG
TTCGGACGGCAACCGGTGGCGANCGCACCT (SEQ ID NO. 496)

.....Rv368T7.seq:.....
CCGGGAGGGACCATCNCGGGCGGCTNCGGCTTCTCTCCGGAAGGTTCTANNGTNNNGCGTTTCNACNCTTCCCGTCGC
CCTGCGACCGCCGAACATTCCGGGTATGGNNGCANCTGTNAGCATCCNGGCCGGGC (SEQ ID NO. 497)

Clone Rv369

.....Rv369SP6.seq:.....
CTCAAGCTTCCGCATCAGATCGCTATAGAACCAGGTGCGCGTCCCCACCGAGTGGCTGGTCGCCTTCCAGCACGATCGT
TACCGCGTTATCGGAATCAAACCTCNCGAACACCTGACCAACGCGCTTGATCGCCTGAATCGATGCGGCGTCGCTGGG
GCTCATCGATACCGAGTGTGCTTTCCGACCACTTCCAGTTGCGGTACGGCGAGATTGACAAAGGCGGTGAAGCCCGAG
CCAGAGCAGGACGATCACCNCCGCAAACCGGCGGATTGCCCCG (SEQ ID NO. 498)

.....Rv369T7.seq:.....
GCTTGGCAGCCTGCGGCTGGGCGCCCTNGAGCTCTTCGATCTGGATCTCCGACTCGAGATGCTCACTTGCCCCGGCG
TGGACGTACCCATTGCGGCGGGGACCCAGCGCCCCAGGTGACCAGCGAGTTGGGCTGCACGCTGACCGGCCCGTCGG
GGTCGACGCGCGGTAACGGTCAGCAGCTCCGANGTCCNNTGATCCCGACCGCAGCTGCCAATGCGCGGCTGGCAGCCG
ACGTGGATGTCCGGGGCCTAGATCGCGGGGACGAGCGGAGACCGGTACCGACGGTCATCACCTTGCCGAGTTTNG
GCCTGCCGCGAN (SEQ ID NO. 499)

Clone Rv36

.....Rv36SP6.seq:.....
GCTTCCGGCTCGTATGTTGTGTGAATTGTGAGCGGATAACAATTNCACACAGGAAACAGCTATGACCATGATTACGC
CAAGCTATCTAGGTGACACTATAGAATACTCAAGCTTGAGCCATCGGGCTATCAGCTGGTTGATGTCCCG
(SEQ ID NO. 500)

.....Rv36T7.seq:.....
CAGGCATGCAAGCTTGTCTATCACATCCGACCACCAACCGCCGACGGCTCGGCAGAAGCCTCCGCATATGGGT
CGAGCAGCAGGGTCGGACTTCTGGGCTGCCAGCGCTCGCGCCGTGCGGACAAACAGCGGGTCGAACCGACACTCC
TTGTGATGTCCACCTATCACCTTCGGTACGCACCCAATCGACCTACGCGGCTAGCTCAGCCCCGATCTTCCAGAGC
TCCGCCCG (SEQ ID NO. 501)

Clone Rv370

.....Rv370SP6.seq:.....
GCTTTTTGAGCGTCGCGCGGGGCGGCTTCCCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACGGATCTGACCGA
AGTCGCTGCGGTGACGCCCACCTCATTGGCGATGGCGCCGACNATGGCGCCTGGACCGATCTTGTGCCGCTTGCCGA
CGGCGACGCGGTAGGTGGTCAATTCCGGTCTACGCTTGGGCCTTTGCGGACGGTCCCGACGCTGGTTCGGGTTG
(SEQ ID NO. 502)

.....Rv370T7.seq:.....
CGANCCTGTTTCGACGGCTACCTGAATCACCCCGATNCCACCGCCGCGGCGTTTCGACGCCGACAGCTGGTACCGCACCG
GCGACGTCGCGGTGGTTCGACGGCAGTGGGATGCACCGCATCGTGGGACGCGAGTCGGTCGACTTGATCAAGTCGGGTG
GATACCGGGTCGCGCCCGGTGAAATTGAAACGGTGCTGCTCGGGCATCCGGACGTGGCGGAGGCGGCAGTCGTCGGGG
T (SEQ ID NO. 503)

Clone Rv371

.....Rv371SP6.seq:.....
NAAGCTTTGTCACACCAAGTGTTTCNACCAGNCGCTCCATCCGGCGAAGTGGATACTCCCAGCAGGTAGCAGGTCGCC
ACCACGCTGGTCAGTGCCGCTTCAGCTCGCTTCGGGCGCTGCAGCAGCCAGTCCGGGAAATAGCTGCCCTGGCG
(SEQ ID NO. 504)

.....Rv371T7.seq:.....
CGCTGGNCGCCGGCGCTGGGCTGCGGTAACCAATTACCACAACACTTTTCGGTAGCCGAACAGCGGCGCGTACCAGCG
AAATGGCACAGCCACCGCAGTCGCGGACATCCCGGAAGATGTGGCAGATTTTCGTGCGGTTCGAGCCGGCGAAGGCCT
AGCGTCATTGTTGCCTGGCAAGGTTGCTGGGCCCGG (SEQ ID NO. 505)

Clone Rv373

.....Rv373SP6.seq:.....
CTCAAGCTTCTCTGCCCCCTTGCCGTTNCGGATNACATCCCGCAGCGACTCGGCTTCGGCGTCGATGTGCAAGTTCTC
GATCAGCTTCTGGATCGACTCCGCGCCCATGGCACCAGGTGAAGTACTCGCCGTAGCGGTTCGACNAGTTCGCGGTAGAG
GTTTTCTGTCNACNATCAGCTGCTTGGGCGCCANCTTGGTGAAGTGCTCCAAATGTCCTCCAACCGGTCCAGCTCAGC
CTGCGCGCGGTACGGATCTGGCGCATCTCGCGCTCGCCGCCGTGCGGAAGTTGCGCCGCGCATCGGCCCTTGGGGCC
(SEQ ID NO. 506)

.....Rv373T7.seq:.....
GTTACACCTACCTACTATGCCNCAATTCNCCGACACGGGTGGCATCAACACGGGCGATAAGGTGGAAATCGCTGGGG
TGAACGTCGGGCTGGTGGCTCGCTGGCAATCCGCGGCAACCGCGTGTGATCGGATTCTCGTTGCCCGGCAAGACAA
TCGGGATGCAAAGCCGGGCGCAATTNCNCCNACACCATTCTTGGCCGTAAGAACCTGGAGATCGAACCCCGCGGTT
CGGAGCCGTTGAAACCAACGGTTTCTGCGGTTGGCGCANACCACTACGCCATACCAAT (SEQ ID NO. 507)

Clone Rv374

.....Rv374SP6.seq:.....
CTCAAGCTTTACGCGGACGCCGCTACACAACACCAAGGAAACGATTGCCTACTGCCGAATCGGGGAACGGTCTCTCG
CACACCTGCTTCTGTTGCGGGAATTACTCGGACACCAAAACGTCAAGAACTACGACGGCAGTTGGACAGAATACGGC
TCCCTGGTGGGCGCCCCGATCGAGTTGGGAAGCTGATATGTGCTCTGGACCG (SEQ ID NO. 508)

.....Rv374T7.seq:.....
TCCNCATGGGATAACGGGTTTAGATTTNACAACGGCACCGTGTTTCTCAACAAGCCGGTCATCAGCTGGGCGGCG
ACAACGGTATCTACTTACCCGCTTTCGCCCCGTACAAGAAAAACCACTAGGCCACCATCGAGTCCAAGAACAACCA
TGGTCCGCAAGTACGCGTCTACTACCGCTATGACACCGCCGAGGAACGCGCCGTGCTCAACCGGATGTGGAAGCTGG
TCAACGACCGCCTCAACTACCTCACCCGACCATCAAACCGATC (SEQ ID NO. 509)

Clone Rv375

.....Rv375SP6.seq:.....
CTCAAGCTTGGGTGTTGCCGATCACCGGAAGCCNATGATCAGCCACGTTTCGCGCCGCCCGGCATACGGCGGCGTAC
CGATCTCCGCGTCATACACCCGCGGTAATCGCCGACGGTGCCGGTTCGCGAGCCGAAGGTGACAACGCTGATTGAAT
CNAGTTCANGTCCAGCGGGT (SEQ ID NO. 510)

.....Rv375T7.seq:.....
TNAACAGCTCGCGGCAGCCACGACCTGCTGCGTCGGATTGCCGGCGGCGAGATCAATTCCAGGCAGCTCCCGGACAA
TGCGGCTCTGCTGGCCCGCAACGAANGACTCGAGGTCAACCCGGTGCCGGGGTCTGGTGCACCTGCCGATCGCACA
GGTTGGCCCAACCGGCGCTTGATGNNNGTCGGCAAGCCCGGAGTNGCCAAACCCAGCGTGATCANGCTCGGCT
CGCGAGTTCGGCGAANAAGTGGCTCGCCTGATCACTACCATCGGCCANGATCTGCGTGTCA
(SEQ ID NO. 511)

Clone Rv376

.....Rv376SP6.seq:.....
GCCANCCGGCTTGGCGTCGACTCCCGTTCNGCACATCATACGGTCCCCGGTACTGTCCAACGCGCCGGTGCGCTAGC
CAAACGTACGACTCTCAGTGATCCAGTTCGTGATCCGGCCGGTGGCGCCGCTGCGCGGGGGCTNATNTACTTCGG
ACTNATTATCTCATCCAAAGGACACCGGGCCGGTGGCTGGAATCCCATGGTGGGATCGGCCACACAN
(SEQ ID NO. 512)

.....Rv376T7.seq:.....
CCGACCTGGTATCTTCCGATAGCGCGCTTGATATCCGGTCTGATCTCCTGCCCTTAACGCCGGATCTCAGCAGGTCC
CCATGCAAAGATCCGAGGTGTCCNGATCTAGGGGTCTCGTCTCCAGATGATGGAGCAAGTCGGCCC
(SEQ ID NO. 513)

Clone Rv377

.....Rv377SP6.seq:.....
CTCAAGCTTCGCTCAGGCGGCGCTGCCGGTAACGTCGCTGACCGGTGCAGGTTTCGACAATGTGGTGCCGGTTCGGC
GGCTACGTGCCATCAAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTACAAACAAATCGCGGTATGC
(SEQ ID NO. 514)

.....Rv377T7.seq:.....
CATCACCTGNTTCATGAACTGGAAGCACCGCAGCGCTTCTTTTCGGCCGCAACATGAGCCAGCCTCTCGTCGGCGGT
CGGGTGAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCCTGAAACCAGCTTCCATATCCCGCGACGAACGA
CGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGCGTTCTCCACCGACCGGGCCCGGTGTGGG
GTGT (SEQ ID NO. 515)

Clone Rv378

.....Rv378SP6.seq:.....
AGCTTAGCTTCCCGCCCCGCAATAGGGCTCCAGCTCATCCGGTGTGACCAGATAGGGGCCAGGGTGATACCGCTGT
CTTTGCCCTTGGCCTGTCCGATGCGCAGCTGGCCCTCCAGCATCTGCAGGTCCCGTGCGGACCACTCGTTGAAAATGG
TATAGCCGATGATCGACCG (SEQ ID NO. 516)

.....Rv378T7.seq:.....
CCNGAACAGAAGCGGNGGTTCTACCGCGGTGTGCGCGCGCGATATCGGCCCTTTTACTAACCGAACCCGATGTG
GGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATACCGCCAGGCTTACCACCTT
(SEQ ID NO. 517)

Clone Rv379

.....Rv379SP6.seq:.....
CTCAAGCTTGCAGGACTCGACAAGCATCTTGACAGTTGTTTTGGCTCGGCATGGTTAGCCAAGGTTCTGCGGTCCCA
CCAGATCATCTTGGTCCGGTAGCGCTCGTCCGGGTATGCTGCCGCCGGGATTCTCGCTGCTATTACTCCCCCGAAGA
ACGCCACCGGTCCAGCGC (SEQ ID NO. 518)

.....Rv379T7.seq:.....
GCNAGGCGGTATAGCTTCCCGTCTGACCGCGACCGCCAGCCGAGAAGCTCGTTTTCCAGTGTTGCTGGGGATTCTC
ACGCTGCTGCTGAGTGCGTGCCAGACCGCTTCCGCTTCCGGTTACAACGAGCCGCGGGGCTACGATCGTGCGACGCTG
AAGTTGGTGTCTCCATGGACTTGGGGATGT (SEQ ID NO. 519)

Clone Rv37

.....Rv37SP6.seq:.....
GTGTGGAACCGTGAGCGGATAACAATTTACACAGGAAACAGCTNTGACCTTGATTACGCCAAGCTATTTAGGTGAGG
CTATATTAATACTCAAGATTGCGGTGAGACATCGGCCCAAGAACC GCCGAAGGCACGGCGGAACGCTGCGGCACA
TGGGGCGACGACCGGGTCCGACTTCTGGGTGTCCAGCCGGATCGCGCGCTCGCGA
(SEQ ID NO. 520)

.....Rv37T7.seq:.....
CACTGTCAGTACATATGCGCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCCGGCGGGTTCATGGCGTCAACCTACC
CAAGCCGAACGCGAAACGAGAACGTGTTCCATTATTAGGGTGTGAGCACCATAACAGATTGCTCACCAGGAACCTCAC
GCAGCACCGGGACGGATGTCAGCCACCACGCCATCTGGGGTGGTAGCGGGGAAATACGGCTAACCGCGCTCCGGTGC
CGGCAGCCAGCGCAGACCCTCGGCGGGCGACACGGCAAACAACGACGACCCATAGTTGTTCTTTGCCGGATGGCCGT
GTTTGCGGACATATCGGGCGGGCGGGCGGGCGCCGAGGTAGTGGCTGAGGCCATCTCGTGCCCGCGGAATGGCC
CCAGCCAAACCGTGTA (SEQ ID NO. 521)

Clone Rv381

.....Rv381SP6.seq:.....
CTCAAGCTTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCAACA
TGAGCCANCCTCTCGTCGGCGGTGGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCCTGACCCTGAAACCAG
CTTCCATATCCCGCGACNAACGAC (SEQ ID NO. 522)

.....Rv381T7.seq:.....
CTCAGAAGCCGCTAGCTGGTAGAGTCGCTGACCGGTGCACGTGGCGNCAATGTGCGCTGCCGGTTCGCG
(SEQ ID NO. 523)

Clone Rv382

.....Rv382SP6.seq:.....
CTCAAGCTTGCGCTCATCAAGCGCGAACAGCGGGCGGTGCGCTGGTCGCCATGACGGGTGACGGGACCAATGACGCA
CCCGCGCTCGCGCAAGCCGATGTGGGGTGGCNATNAATACCGGCACCCAGCGGCCCGGGAAGCCGGCAACATGGTC
NATCTCCACTCC (SEQ ID NO. 524)

.....Rv382T7.seq:.....
ACTTCTATTTGCGACTGGTGTGCTGTGGCGCATCCGACTGCCGGCGTGGTCAAGGCCGGCCAGTTGTGGGATNCCACA
GGCAC (SEQ ID NO. 525)

Clone Rv383

.....Rv383SP6.seq:.....
GCTTGTCGTATTCCGTGGCACTGTCAGACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGT
CATGGCGTCACCCCTACCCAAGCCGAACGCGAAACGAGAAGCTGTTCCATTATTAGGGTGTGAGCACCAATACCAGATT
GCTCACCAGGAATCAC (SEQ ID NO. 526)

.....Rv383T7.seq:.....
CGATATTCGTCGGCCGCGTTGTCTCGACTGGGTGCGGT (SEQ ID NO. 527)

Clone Rv384

.....Rv384SP6.seq:.....
GACCTCGGCCACCAAGCCGGACGCGACCGTTCGAGGTGGCGATCCGGCTTGGCGTCGACCCGCGTAAGGCAGACCACAT
GGTCCGCGGCACGGCCANCCTGCCACACGGCACTGGTAAGACTGCCCCGCTCGCGGCN (SEQ ID NO. 528)

.....Rv384T7.seq:.....
CCGGAAGTCTAGGGGACGACCTACTCAGCGCAAATGTGCTAATGTGAGTCCGCCCCACCAGGGCAGATCAACCCAT
GTCGATGATGACCTACCCGGATACCGGATTGGCGGT (SEQ ID NO. 529)

Clone Rv385

.....Rv385SP6.seq:.....
AGCTTCAGTTCCTCCACGACGCGTTCCCAAATGAATTTCCCGATCCCAATCTCGGTTAGATACAGGTGCGCCATAC
CCCTTACTTCGGNAACGCTGGCGGATTGGCCCTGCCGCTG (SEQ ID NO. 530)

.....Rv385T7.seq:.....
CCGCCTACGGGTGGAACATGCATCCCGAGACCGATGCTCGAGCGCGCACCCCACTCGCCGATGGCCGGAACCGGCTGG
TTACCCGGGTGGCGGCTGACC (SEQ ID NO. 531)

Clone Rv386

.....Rv386SP6.seq:.....
GCGGCTGGTTACGACTCCCTGTTGTGATGGACCACTTCTACCAACTGCCCATGTTGGGGACGCCCCGACCAGCCGATG
CTGGAGGCCTACACGGCCCTTGGTGCCTGGCCACGGCGACCGAGCGGCTGCAACTGGGCGCNTTGGTNACCGGCAAT
ACCTACCGCAGCCCCGACCCTGCTGGCAAAGATCATCACCAGCTCGACGTGGTTAGCGCCGGTCGAGCGATCCTCGGC
ATTGGAGCCGGTTGGTTTGGAGCTGGAACACCGCCAGCTCGGCTTCGAGTTCGGCACTTTCAGTGACCGGTTTCAN
(SEQ ID NO. 532)

.....Rv386T7.seq:.....
GCCTTTCCGCACAATCTGTACCCAGGACCNCTAAAAAATCGAATACGACGGCGTCGCCGACTTTCCGCGGTACCCG
CTCAACTTTGTGTCGACCCTCAACGCCATTGCCGGCACCTACTACGTGCACTCCAATACTTCATCCTGACGCCGGA
CAAATTGACGCAGCGGTTCCGCTGACCANTNNTGTGGTCCCACGATGACCCAGTACTACATCATTGACGCGGAGAAC

CTGCCGCTGCTAGAGCCACTGCGATCGGTGCCGATCGTGGGGAACCCACTGGCGAACCTGGTTCAACCAAACCTGAAG
GTGATTGTAACTGG (SEQ ID NO. 533)

Clone Rv387

.....Rv387T7.seq:.....
GCAGACCAACAAGATGCATCGGGATCATACGCCGTCAACTACCCGGCCAACGGTGATTTCTTGCCCGCCGCCAC
(SEQ ID NO. 534)

Clone Rv388

.....Rv388SP6.seq:.....
CTCAAGCTTGCCAAAGAGACCTCGTCCACCAAGCNGGACGCGACCGTCNAGGTGGCGATCCGGCTTGGCGTCCACCCG
CGTAAGGCANACCANATGGTTCGCGGCACGGTCAACCTGCCACACGGCACTGGTAANACTGCCCGCGTCGCGGTATTC
GCGGTTGGTGAAGGCCGATGCTGCCGTTGCCGCGGGGGCGGATGTTGTGCGGAGTGACAATCTGATCGANAGGATT
CAGGGCGGCTGGCTGGAATTCGATGCCGCGATCGCGACACCGGATCAGATGGCCAAAGTCGGTCNCATCGCTCGGGTG
CTGGGTC (SEQ ID NO. 535)

.....Rv388T7.seq:.....
CCACGGCGTGATCAAGGTACCGCGCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTGCGCGTTAGCGC
CGGATTCACACACATCCCCTTGCGAAAGTCCGTTGGGTGCAATGATGTAGCGCTTCTCCCCATCGAGATAGTGGAGCA
ACGCAATCCGTGCGGTACGGTTCGGGTCNTACTCGATGTGCGCGACCTTGGCGTTGACACCATCTTTGTCATTGCGGC
GAAAGTCGATCATCCGGTAAGCGCGCTTATGACCGCCGCCTTTGTGCCGGGTGGTAATCCGGCCATGCGCGTTGCGTC
(SEQ ID NO. 536)

Clone Rv389

.....Rv389SP6.seq:.....
GGCGGCTGCGTCGGCGAGATGATCGCCCGGTGCCACCCCGATCCGTGCGCTCGGTGAGCGCCAACGTGCTTCCGGTCC
GGCGACCACCATGTCGATGCGCCGAC (SEQ ID NO. 537)

.....Rv389T7.seq:.....
GCAATCGCCTTGCGGTCGCGGGTGTACCGGTGATCATCNCGGNGCGGATGCTCATCNCGGCGCATTTCTGTCNAAT
CGTTCCCGTATGCCACCTTGACGATGTCCTTCATATGGACCACGCCGATGGCCCNCGCGCTNCTG
(SEQ ID NO. 538)

Clone Rv38

.....Rv38SP6.seq:.....
CCGGCTCGTATGTTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAG
CTATTTAGGTGACACTATAGAATACTCAAGCTTCCACATCGGTATGCCAAAGCATTGCGCCGCTATCGATTTGCGCGT
GGCATCGCCAAGGTGGACTTCTTGCTCAGCGACGAGATCCCGTGGTCCGATCCGCGGCTGCGCGGGGCTGCGACCGTG
CATCTCGGCGGCACCCGTGACCAGATGGCGCGCGCGGAGGACAGCTCGCGGCGGGACGCCACGCCGACTGGCCGATG
GTGCTGGCCGCGTGTCCGCACGTGCGCGACCCCGGCCGATCGACGAAACCGGCCGCGCTCCGTTCTGGACCTATGCC
CACGTGCCGTGCGGGTCCACGCTCGACGCGACCGAGACCGT (SEQ ID NO. 539)

.....Rv38T7.seq:.....
CGCGTCCACCGCAGCGTGAGATTGGTGGCGCCATTCTGTCGTGGTGTAGCTGCTGTTGGCGGCGTCGCCGTATTGTGCG
GGCCAGCCTTGTGCGGGGGCCGCTTCTACCCACGAGTGGGCACTTCCGCAACCGCCAGCTCGACCGCGATTACGGCG
GCCGCAACGGCCGCCGGAAGGCGTCTCGCAAGCGCCTTATCCTTTCCGAGGTTCCAGATCCTTCCGCTACGTGGGTC
GCTCATCGCGGGGCCCCGGCCGAATGAGTACAGGTGAGGGTAACCGCTACAAATGAAGTTGGTCAGTGCTGGCCAACTG
TGTAATGGTTGCCCGGCTCGGGTCACACGTACATTCTGGCAAGCGGGCGAGATTGCTTCTCGCGTCTTGGCCG
GTGGCGGTTCCCGGTTGTCCGTGGGCGTGTGCTGACGTGGTGAAGTGTGCTGAACTCCTCAGTTTGGGCT
(SEQ ID NO. 540)

Clone Rv390

.....Rv390SP6.seq:.....
CTCAAGCTTGCGCTGGATCTGGCGGCTGAGCCTGTTCTTGGGCAACATGCCGAGGGATCGCCTTTTCCACCACGCGGT
CGGGGTGGCGTTGCATTAGCTCACCGATGGTGCCTTGTGCGAGGCCCGCGGATACCCCGAGTGCCGGTAAACCATCT
TGTGCTGCAGTTTGTGCGCGCTGATGGCGACCTTGTGCGCGTTGATCACNATGACNAAGTACCGCCATCGACATTGG
GGCGCAACGTGCGCTTGTGCTTGCCGCGCAGCAGGTTGGCCGCCGACGCGCAAGGCGGCCAANCACACGTC
(SEQ ID NO. 541)

.....Rv390T7.seq:.....
TTTGGGATGGGCAAAAAGGCCAAGCNC CGCGTGGCCACGAACGCCGGGAGGGACAATCTCGGGCGGCTAGGGCTTCTC
GCGGGAAGGCCCGAACGTACGGCGTTTCAACACGTGCGCTCGCCCTCCGACCGCGAACATTGCGGGATGGCAGCAACC
TGGTAGCACCTTGGCCGGGCGATGATCTGCAGCGTCGCCCGGGTAGTCGCCGCCCGGGCGGCTACAGTCTGAAACGC
GATGACCATCGATGTGTGGATGCAGCATCCGACGCAACGGTTCTACACGGCGATATGTTGCGCTCGCTGCCCGGTG
GACCGGTGGGTCTATCCCGGA (SEQ ID NO. 542)

Clone Rv391

.....Rv391SP6.seq:.....
CTCAAGCTTCGTCATAAGACCATGGTGCCTTTCTTTACCCGTCANAGTCGGGGGCATCCGCACCGGCTCGCATCG
CATCATCTCCACGACGGGCCGCTCATCAGCTTGGGCCATTCAATGTACTTGATACCCCGCGCTGCGGGTAGGCCA
CTGCNACATTCAAACACGGGTGTACACGGTGAATANTGTNANATGGGCTCTGATCAACCGTCNAAACCCGGTTTC
(SEQ ID NO. 543)

.....Rv391T7.seq:.....
GAATTCTGCGTGACCGCTATGGGTGCGAGCAGCGGTGGCGCCGCACACCCCACTGGCCCGGGTGTTCGCCCCGA
ACCCGGATCATGGTGAGCGAAAAGGAGATTGCGCTGTTGATGCTGGGATTGCGCACCGCGAGGCCATCGACCGATTA
CTCGCCACCGGGGTGCGAGAGGTGCCGAGTCCCGCTCCGTCGACGTCTCGACGATCCATCCGGCTTCCGCCGTCGG
GTGGCGGTAGCCGTCGATGAAATCGCTGCCGGCCGCTACCACAAGGTGATTCTGTCCCGTTGTGTGCAAGTGCCTTTC
GCGATCGACTTTCGTTGACCTACCGGCTGGGGCGTCTGCACAACACCCCGGTGAGGTGCTTTTGTGTCAGTTGGGC
GGAATCCGTGCTCTGGGTTACAGCCCCGAACCTCGTCNCGGCGGTGCGCGC (SEQ ID NO. 544)

Clone Rv392

.....Rv392SP6.seq:.....
GCAGTTGGGAATCGCTCTGCAGCAAACCANTATTCTGCGCGACGTTCTGAGAGGACTNNTTGAATGGACGGATCTACCT
GCCGCGCGACGAGCTGGACCGATTAGGCGTACNCTCCGCCTGGACGACTCCGGGGCACTCGATGACCCCGACGGACG
GCTCGCGGCACTGCTGCGGTTTANTGCCNACCGCGCCGANACTGGTATTGCTGGGACTGCGGCTGATTCCACACCT
CGACCGCCGACGCGTGCTGCTGTGCGGCCATGCTGCGCATCTACCGCGCTCNGCTCGCCTTGATCAGACCATCGCC
GGCGGTGCTTACCATCGGCGAATCTCTGTTGCGGACTGAANAANGCCCAAGTGGCGGCGGCGAGCACTGGNCTCTT
CGGTAACCTGCNGACCGCCCATTTGGACCGCTACCG (SEQ ID NO. 545)

.....Rv392T7.seq:.....
TTGATCTGGACGTCTGAGACGGTGATCGGNCCGAACCTGAATTGTCCGGTAATGCCAGCGCAGAAAGCANGGTGGTG
GCCGGGGCGGTGAANCCGGCGTCGGCGGCACCGTCGAAGTCGATGTGGATTGCCGGAATGGGGATGTCGGGCACGGCG
AAGCCGTAGTTGCTTGTCCCGTGAGGCCCANGTGGATGGGGGGAAGGATCGTGGTGTCGGGATGATAATGGGGCCG
ATGCCGCGGTTGAAGTCCAGTGGATCGGGAATTGCGGAATCGTGATGCCGACGTTGAGGCCGAACAGGCCCTCCAAG
TTGCCTCGCCACNAGATGCCGTTGCTGAAGTTGCCCGACATGAGGGCGCCGGTGTCCACATTGCCCGAATTGGCGACG
CCGGTGTGGC (SEQ ID NO. 546)

Clone Rv393

.....Rv393SP6.seq:.....
CACGTAGGCGCGCTCCATAAATNACTCCGCCGCGCTTCGCACATCCTCGTANCGATCCTTGGCGAGCAGGTCAACCGG
GCGCTGCCCCGTCNAGGAGCCGTTTTTGGCGTGACCCACTGGCCGACACCTCGGGGGTAAGCGAATCCGAGAGCAG
GAGGACNAGGTACGAANCTGCCCGAGCCGGTCGTACCGCTCAGGGCGGATGTGCCCGTCCGCCACCCGCGTACCGC
CCGATCGGACACCTGTATGACCGCGGCGACNTCGACCTGGGTGACGCCGAAGGGTTTCAGGGCATCNACNATCTCGCT
GGCCTCGACCGCCCGGTCCAGGGTGACCGCCATCGTGTTCTCCGCAACTTCCGGTTCTACTACCGTAACGCTACC
G (SEQ ID NO. 547)

.....Rv393T7.seq:.....
CGGGGAACGGTCTCGCACACCTGGTTGCTGTTGCGGGAATTACTCGGACANCAAACGTCAAGAACTACGACGGCAG
TNGGACAGANACGGCTCCCTGGTGGGCGCCCCGATCGAGTTGGGAAGCTGATATGTGCTCTGGACCCAAGCAAGGAC
TGACATTGCCGGCCAGCGTCGACCTGGAAAAAGAAACGGTGATCACCGGCCGCGTAGTGGACGGTGACGGCCAGGCCG
TGGGCGGCGCGTTTTGCTGCGGCTGCTGGGACNCTCCGACGAGTTACCGCCGGGAGGTGCTGCGCTCGGCCACCGGG
CGAATTTCCGGTTCTTCGCCGCGCCCCGGGATCCTGGGACCGCNGGCGCGCGCTGTT (SEQ ID NO. 548)

Clone Rv396

.....Rv396SP6.seq:.....
CTCAAGCTTTGTCCGACAAGCGTTCGCCGGCGGTGAGCAAGCGAACGTGCGTTGGCCCACTGCGGGTCGATATTGCCG
CCAGGGA (SEQ ID NO. 549)
.....Rv396T7.seq:.....

CGTCAGCACGGCGACGTGCGGNTACGCCGAGCAGTTACACAATCGCTCTGCAGCAAACCAATATTCTGCGCGACGTTCC
GAGAGGACTTCTTGATTGGACTG (SEQ ID NO. 550)

Clone Rv39

.....Rv39SP6.seq:.....
CTGCATCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTAC
GCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCGCGCAGCGGGGTTGACCCGGTTCACGCCGTCATAGC
TGGCCAATCTGGCATCGTCGATCANCATGTGGTGGGGGTGACCTCGGCGGTGATCGAAATACCCTGGTCCCTTATCCC
ATTTTCAGGATTTTCAGCGGTGCCCGCGGCCGACGCGTGACAGATGTGCACCCGGGCGCGGCGTCACGGGCCAGCAAGG
CGTCGCGGGCGACGATCGATTCTCGGCGGCCCGCGCCATCCCGCCAGGCCAGCCGCGCGCCATGGGTCCCTCGT
CGCGCAGCGCGCCGACCGTCAGCCGGGGCTCCTCGGCGTGCTGGGCGATCAGCACGCCCAAACCGGTG
(SEQ ID NO. 551)

.....Rv39T7.seq:.....
CCGACGCGCACTACGTGCTGGTGTCCACCCGCGACCCGACCCGGCAGAGCTACGCGCTACCGCATCGTCGATGGCG
CTGTCCCGAGGAACCTGTCAATGTCTGTCGAGCAGTCTGAACCGTTCCGAGAAAGGCCAGCATGAACGTCACCGTAT
CCATTCCGACCATCCTGCGGCCCCACACCGGCGGCCAGAAGAGTGTCTCGGCCAGCGCGCATACCTTGGGTGCCGTCA
TCAGCGACCTGGAGGCCAGCTATTGCGGCATTTCCGAGCGCTGATGGACCCGTTCTCCCGAGGTAAGTTGCACCGCT
TCGTGAACATCTACGTCAACGACGAAGACGTGCGGTTCTCCGGCGGCTTGGCCACCGCGATCGCTGACGGTGACTCGG
TCACCATCCTCCCGCGCGTGGCCGGTGGGTGAGCGGACACATGACACGATACGACTCACTGTTGCATGCCTTG
(SEQ ID NO. 552)

Clone Rv3

.....Rv3SP6.seq:.....
TGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACG
CCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCGCGGGAGGGTGCATGGCCGACTCGGATTTACCCACCAAG
GGGCGCCAACGCGGTGTCCGCGCCGTGCGAGCTGAACGTTGCTGCCCCGCTGGAGAACCTGGCGCTGCTGCGCACCTG
GTCGGCGCCATCGGCACCTTCGAGGACCTGGATTTCGACGCCGTGGCCGACCTGAGGTTGGCGGTGGACGANGTGTGC
ACCCGGTTGATTGCTCGCTCGGCCTTGCCGGATGCCACCCTGCGCCTGGTGGTGCATCCGCGAAAGACGAAGTTGTGGTG
GAGGCTTCTGCTGCCTGCGACACCCACGACGTGGTGGCAGGGCAGCTTTAGCTGGCATTCCT
(SEQ ID NO. 553)

.....Rv3T7.seq:.....
GGAAACACCGNCGCCGTCTGTTGCCACCAACACCGCGACCGAGCACCGTGACCCGGACCGGGTGCCGCGCGAACCAGTC
TTGGCCAATTGCCGCGGCACCAAGCCGTGCGCGCCATGGCGAACAGCACGCGGCATTGCCCGAGCATCAACACCATC
ACCACCGTGGTAAGCCCGGCCAGCGCGCCGACGAGATGATGCCGCTGGCCAGTACACCCGTTGGCCTGGAACGCG
GTGGCCAGATTTGCCGCGCCGCGGCCCGGTACGGTCCGAGTTGGGTGATGGAACCATGCCCGACGACACCCGAT
ACCCGACGTAGAGAAGGGTCACGACCCCGACGACGCGAGAATCCCTCGAGGGACGTCCTCGTTGAGGACGCTTGGTC
TCCTCGGCCATGGTGGCCACGATGTCAAACCCGATAAACGCGAAGAACACGATCGATGCCCGGCCAGCACGCCGTA
(SEQ ID NO. 554)

Clone Rv40

.....Rv40SP6.seq:.....
CCTGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTAC
CGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGTCTCGGGCGTGGCCTCGGCCAAGAAATCGTCGACGC
CGGCCTCCTGTGAATCGCCTTGGCGGTGCGCGGTTGTACCGGTGATCATCACGGTGCGGATGCTCATTGCGCGCA
TTTCGTGCAAGCGTTCCCGTATGCCACCTTGACGATGTCTTCAGATGGACGACGCCGATGGCCCGCGCGCTGCTGT
TATCGGTCCATTCCGCAACGACTAGGGGTGTCCCCCGCGGAGCTGATGCCGTCGACAATGGCACCCACCTCCTCAG
TGGGGTGGCCACCGTATCGCAAACCACTTCATCACCGCAGCCGCGGACCTTGGCGATCCGAACGGATGCGCTC
(SEQ ID NO. 555)

.....Rv40T7.seq:.....
TTCGTTGATGGCGCCCGCCCGGCTACGGTTTACCTGTGGGTGTGCAATTGGGGTCAAATTCGAGGTGCGGCGCGT
AAGAGTGGTCATCTGCACCGCCCGGGGCGGAAGTGCGCCGGCTCACACCGCGCAACACCGACGCTGCTGTTGCA
CGGCCTGCCCTGGGTATCCCGCGCGCATGACGACGACGAATTCGCCGAGCTGCTGGCTTCCCGCGGTGCGGAAGT
GCTGTTGCTGTGCGACCTGTTGACTGAGGCACTACATCACAGCGGGGCGCCCGCATGCAGGGGATGCGCGCTGCCGT
CGACGACCGCGGCTGGGACTGCCGCTGGCGCAAGAACTTTCGGCCTACCTGCGTATCTCGACCCAAAGCANGTTGGCG
CATGTGCTGACGCCGCGATGACTTCAACGAAGTCCNTCCGACACGCCGAACGAAGTGTGCTTGGTGTGCGTATGC
(SEQ ID NO. 556)

Clone Rv412

.....Rv412SP6.seq:.....
GCGGCGAGTGTGGTGGTGCCGAACACGAATCCAACGACGCACTGGCGGAGAGATACCACTTGCTGTACTGGAAGCAC
GTGCTGATGATCTCCCGTGAATGTGCCTCGCCGCCGTCTATCGAAAACAGTGAGCATGCTGCG
(SEQ ID NO. 557)

.....Rv412T7.seq.....
CAACCGCGCTCGGCGCGTCTGGGCCTTCCGCCGGCTCCGCCGACAATTCTATCTCTGGATCAGCGGGGCTCTCCGGGC
CGGCCTCCGCGAACTCAACAGGCCGCGCCTTCCGGCCGAAACATTCCCTAGCCATATATGATCGCACCTCGATACAG
ATCTGGCGCAACACCGCAAAGCGTCCGACGGGCCAACCTCCGCAATTCAGGTATCCGGG

(SEQ ID NO. 558)

Clone Rv413

.....Rv413SP6.seq.....
GAAGGTGCGCGAAGGTGTGGCTGGNTGCCGATCACGAATCCAATGATGCAGTGGTGGGAAGATATTAGCCACTTGCTG
TTCTGGAGACAGGTGCTGATGATCTCCCGTGAATGTCCCTCGACTCCGTCTATCGAAATCTGTGAACA

(SEQ ID NO. 559)

.....Rv413T7.seq.....
TCCTGCGCTCTGGGCCATTCTCGGGTCTGCCGACAATTCTATCTCTGGATCTGTGGGGCTCTCTTGGCCGGCCTCNGC
GATCTCTTCANGGCGCGCCTTCCGGCCGAAACATTCCCTATCCATATATGATCGCACCTCTATACACCGTTTGGCGGC
AACACCGCAAAGTGTCTGTCTG

(SEQ ID NO. 560)

Clone Rv414

.....Rv414SP6.seq.....
AGCTTTACGCTGGCGTATCAGCGTTGGGGCCGCTGCCATTTGGTTCGCCCAACGCGTTGCCAGCTCCCTGCGCTGTCA
GGGCTTGCGCGCCAACTGGCCACCGCAACAACTTGGCTGAGCTTGATC

(SEQ ID NO. 561)

.....Rv414T7.seq.....
CTCTATCTGGCGTCACATTGCAATCTTTAGATTGCAGATATCGATAAAATCACCCGCGCGACAAGACCGCCATGTCA
TCCTTTGATGTTATTTGCGCCGGCCTGGGGAAAGCGCAACGACGTTGCCTACACGTTCCGCGCT

(SEQ ID NO. 562)

Clone Rv415

.....Rv415SP6.seq.....
AGCTTTNCCTTGCACTCTGCACCCCGATCCACGTGAGCCACGTTCGCCGCTTCTCCACCAAGAAGTTGCGGGCATTCTCCT
TGCCCTGGCCGAGCTGCTCGCCCTCGTAGGTGAACAGGCACCCGACTTGGCGATGAGGCCCTGATCCACACCCATGT
CGATCAGCGAGCCCTCCCTGCTGATTCCCTTGCCGTAGAGGATGTGCAACTCGGCCTGCTTGAAGGGGGCGAACAGT
TGTGCACGACAACCCCTTCGGCGACGAGGGTGTGCACTTCCTCGACCTCGAGGTCGAACGTTTCGTGCCCGCCGCGTTG
GCAGCACTTCTCGGATCACGGAATAGCGGANTTCTTCCGCCAGCATGTCTGTCAGGAATTTGTCTATCCAGGGCATCCG
CGAGCGCCTGCACGCG

(SEQ ID NO. 563)

.....Rv415T7.seq.....
ACTGTNAGGGAATGCTTCGCAGCATCTACCTGCAGTCGCTTGTGCATAAGCGGACGGCCCNACCTGTTCTGTTCCG
GGACACCAGACGCGGGAGCACCGGCAGTACGGCGAAAGTTTGAAGCGGAAGGAGTTGCGCAAATCGGGGCGCCCAAC
ACCCGTCCGCAAGACGCGGTCAACGACCTGTTTCAGGCGATCAGGGTCACCGACTCACCTGCACTGAGAACAAGCGAT
CTGCTGATCTGCCAGAAGATGGACATGAATGTCCACGGCAAGCCTGATGGCCTGCCGCTCTTCCGGGAATGTTTGGC

(SEQ ID NO. 564)

Clone Rv416

.....Rv416SP6.seq.....
TGAATTATGATCCCGACACAACCTGCATCANTTTAGCCGCGTCGNGATGCTATCCGCCGACGGTTTGGANCNGGTCCGT
GTCGTTTCGTGTTGATCTCACCCGAAGTTGTGTCCGCCGCGCGGGGATCTAGCGAACGTGGGATCGACAATCAGCGC
CGCCAAACAGGCGGCGAGCGGCTGCGACCACGCGAGGTGCTGGCCGCGGGCGCGATNAGGTGTCAGCGCGCATCGCGGC
GCTGTTTGGTATGTACGGCCTGNAATATCCGGCGATCAGTGCGCAAGTTGCCGCGTATCACCANCACTCCGTGCG

(SEQ ID NO. 565)

.....Rv416T7.seq.....
AACGGGGACCNAAGAAACATTCAANAACGAGGGTTCGTACCAACGTCGAAACCGACGGTTGCCAGCGGGCCACG
ATATTGCGTGCTCGAGGGTCCGCTGTACCCTCACCGAACGTGAGTCCACACCGCGGAGGCGGGCGACTCTGGCGTGC
TTAGCAGCCGAGCTCAAGGTGTCCCGACCACTGTCTCGAATGCTTTAAACCGACCGGATCAGCTCTCCGCCGATCTA
CGTGAACGAGTGCTTGCCACGGCCAAGCGACTGGGCTATGCCGACCGGATCCGGTGGCGCGATCGTTGCGGACCCGC
AAAGCCGGTGCGGT

(SEQ ID NO. 566)

Clone Rv417

.....Rv417SP6.seq:.....
AGCTTTGGAGCCNCNCCGANCCNCCGGTACGCCCCGCCACCGCCGTACCCGGCACCCGACCCCTTTGAGCCGTTGCGC
GTGGCCGCGGTGGANCTGGCCGACGAGGGACTGATCGTGCTGGGCAAAGTGGTCGATGGCAGCGTGGCCGCGGATCTG
AAGGTCGGCATGGAGATGGAGCTGACGACCATGCCGCTGTTGCGCGACNACGACGGTGTGACGCGCATCGTCTACGCG
TGGCGGATCCCATCGCGCGCCGGCGACNATGCANAGCGCANCATGCTGAGGAGCGGCGCCGATGAGGATGAGCGCGC
CGGAACCCGTTTACNTCTGGGTGCCGGTATGCACCCGTGGGGGAAATGGGGTAATGACTTC

(SEQ ID NO. 567)

.....Rv417T7.seq:.....
TTCTCNCATCGTTCTGACTNNGATGGGACGCTGCTGCCCCGAGGCGATCCTGGCCAACCGGCTCTCGCCGGCGCTGACC
TTCGGCGGGGCGAACCTGAACCTCTTTCCGATGGGCGCTTGGGCGCAAACGTACCGGGGCTATCTTCATTGCGCGTCAG
ACGAAAGATATTCCCGTCTACCGCTTCGTATTACGTGCTTACGCCGCGCAGCTGGTGCAAAACCATGTCAACCTCACC
TGGTCGATCGAAGGGGGTCCGACCAAGCGGGCAAGCTACGGCCACCGGTGTTGCGGATCCTGCGTTACATCACCAGT
GCGGTGACGAAATCGACGGTCCCGAAGTGATTTGGTGCCGACCTCGATCGTGACGAACAGCTGCACGAAGTGGA
GCCATGACCACCGAAGCCTATGGCGCCGTGAA

(SEQ ID NO. 568)

Clone Rv418

.....Rv418SP6.seq:.....
TTCTTCCGGGTACCGCTGATCGGCGGCACCATCACGCACCCGGTGCAGGGCGAGGCGGCCCGGCTGTGGTGTGCTA
CGGCCGCGCAGCCCGGTACCGGTGTGATCGCCGGTGGTGCGGCCCGCGCGGTGCTGGAATGTGCGGGGTGCACGAC
ATCTTGGCCAAAGTCGCTGGGCAAGTACAACGCGATCAATGTGGTGACGCCACCGTGGCCGCGCTCAAGCTGCTGCAC
CGTCCGAGAGGAGGTGGCGGCGCGCCGCGTTTGCCAATAGAAGACGTCCCCCGCGCGGGATGCTG

(SEQ ID NO. 569)

.....Rv418T7.seq:.....
GTCGAAAGTGACCATCTCTACCTTGAGTGCCATACCGCCCCGACCTATGCCTCGGATAGCTCGGCGGAAAGAAACGCT
TGCACTGCCGCCGAATAGGCGGCTACGTGCTGAGCGCCCATCAACTCTCGCGCGGAGTGCATCGCCAGCTGGGCGGCG
CCGACGTGACCGTGGGGATTCCGGTGCGCGCGCGCGGCCAACGGCCCGATCGTCGACCCGACGGCAGATCGGCGCGA
TGTTCTGTAACGCTGCATAGGCACTCCCGCGCGCTGGCAGGCCAGTTGCGAAACGCCCCCGCGGGTGCCTTCCGTCGG
TTGGCTTTACCGCAAATTTGGGGTTGCCCT

(SEQ ID NO. 570)

Clone Rv419

.....Rv419SP6.seq:.....
AAAGCCACGGAACGATTGCCTACTGCCGAATCGGGGAACGGTCTCGCACACCTGGTTCGTGTTGCGGGAATTACTC
GGACACCAAACGTCAGAAGTACGACGGCAGTTGGACAGAATACGGCTCCCTGGTGGGCGCCCCGATCGAGTTGGGA
AACTGATATGTGCTCTGGACCAAGCAAGGACTGACATTGCCGGCCAGCGTCTACCTGGAAAAA

(SEQ ID NO. 571)

.....Rv419T7.seq:.....
TTTCGCCACCGCNAGGTCGTGCGGTTCCAGAAAAGCGTGGTTTCGCCGGGCGCGAGGATTCGACGGTCCAACTGACC
AGCCGGTCCCGCCACCCGTTAGGCAGGATCGCGGTGTCTATATGTTGCCCCCTCGGCATAAACGCCATTGCTGCGGTGA
AAATCGGACATCTCGCCGATTGCCAGTCTACATGATCCGCTTTGTCCCGCGCGGGTCTTGACAAACGCGATGTGN
GCCTCCTGGGAAGCGGTGGC

(SEQ ID NO. 572)

Clone Rv41

.....Rv41SP6.seq:.....
TCGCCAAGTGGATTCTGTCTACCNACGAGATCCGTGGTCGGATCCGCNGCTGCGGCGGGCTGCGACCCTGCATCTCG
GCGGCACCCGTTACCAAATGGCGCGCGCCGAAGCAGACGTCTCGGCGGGACGCCACGCCGACTGGCCGATGGTGTGG
CCGCGTGTCCGCNCGTNCAGACCCCGCGGCATCNACCAAACCGGCGCGCGTCCGTTCTGGACCTATCCACGTGCC
NTCGGGGTCCACGCTCGACGCGACCGANAACGTAAACAGCGTCTCGANCGGTTGCCCCCGGCTTCCGTGACATCGT
GGTGGCGGCGCGCGCGT

(SEQ ID NO. 573)

.....Rv41T7.seq:.....
GTACCGTCACCATGATCGCCCCATCGGCATCGGTGAGCTGATAGATCCCAGCCGGTTTCGCCAACCCCGGAGCGATC
TTGGCGCGCTGCTNGTNCNTGANACNTAGCCACCAACAGAGCCCGGTGTGCGACAAGANGACTGATCGGATCTCT
CCGGACACNTCGAGGGGTGNTCAGGAGNCCGGCGCCACCCCGAGGTAAGCCTCCGCCCAGCCTCACACCGCGACCC
GGTATCNCAAGTCGCGCAATAANCCACACCTCCTCGGACCCACGTTGTATGCGGCTGGT

(SEQ ID NO. 574)

Clone Rv42

:Rv42SP6.seq:::

ATACTCAAGCTTAGACCTCACTGATGTGGCGGGACGCGGGAGATAACCGCGGTTTCGAGCCGTTCAACAGTGGTGGTTC
CCACACCAGTTGTTTGCCTTTGCGAAGTAAAGCGATTGATTTGCTCGAAAAGAGGGCTGGCTGCTCGTGAGGGACAT
CCATGGCCGATACCTCAGCGATCTCAACGGTCAAGCGACTGCATGTTTGGCGCAAGGTATCGCTAAGCATAGGTTTCGT
GACGGATTTGACAGCAAGAGCTTTCCAAAGATTGCTGTCCACATANTGATTTCGCATCTCTACACCTCTTCGCCGGTGC
TGTCAGAGCCATTGGAATCAGTTATCTCGCTCGTGTGGAANAAATTTCCAGCCTGCGTTGGACAAACCGCGTC
GCCAAAGCGGT (SEQ ID NO. 575)

:Rv42T7.seq:::

AGCTTCCCGAGAAACAGTGCATTCCCTAAGCAGCCCGTTGTACGCCGATGAGTGAAGAGTGCACGCAATCGCCGGAA
TCCGGCAAAGCCCTGCACAAGCGAAATCAACCCGAGGGCTGACAAGGCAACGTCGGTGATCCGTACCGCCTGGTTGGA
CAAACGGCAGAAGGCGGCTCGTCCGGTCCATCTACGCCGAGCACACTGGTGATAGCGCGCATCGGCATCGGTGCGGC
CACGGTGGAGACGACGTCGCGGGGCTGTGGGTGAGTAACCCGCCGACCAGTTCTCGGGCAAGCTGGTCGACCATCGG
GCGCCACGTCTCAACGCGCCACGCGCCATACCTGGTGCAGTTGCTTGCATCCGGGTGTCGCCGCGGCGGATCGGA
CGTCGCAGAAACGCAGCCACCCGTGAGAAGTGACCCACGGCGCTGGACACGTGTCTGGTTAC

(SEQ ID NO. 576)

Clone Rv43

:Rv43SP6.seq:::

CGGCCGGGATGTGCGCAATGGCAGGTTGTGCGCCGGCTTGATGTGCGCGTTAGCGCCGGATTCCACCACATCCCCTTG
CGAAAGTCCGTTGGGTGCAATGATGTANCGCTTCTCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGTT
CGGGTCGTACTCGATGTGCGGACCTTGGCGTTGACACCATCTTTGTCATGCGCGCGAAAGTCGATCATCCGGTAAGC
GCGCTTATGACCGCCGCCTTTGTGCCNGGTGGTAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGCG
CACCAGCGACNTCTCCGGGGTTGACCGGGTGATCTCGCGCAATCAGATACGCTGGCGCCGCGACGACCAGGCGTCGT
GGGCTTGTAATTGCGAATTGCCATGGTCTAATCAGGTCTTTCTCTCACCTCTCGTCGCCGGGCTAGGGCGCATTGCT
GCTCCT (SEQ ID NO. 577)

:Rv43T7.seq:::

TAGCGGTGTAACCAACTCCCGGGTCACCACCCGCAAACTCTTTCGGGCAACAGCACCGTTCGACGCGTCAACCGGGCTG
CCCGGAATCCTGTGGATGGGCATCGAGTGCATGGTCACGACGTCCCCGACGCGGCGCGGTGGCAACGACAAGTGGCCCG
GATGCACCACAAATGACGGCCGCACACCGGTGGGGACGGCCAGCACGAGAGCCGTGTCCCGGAAGTCGACGCTAATGC
CGTAGGCATTGGCCGTCAACAGGCGACGCCCCGCGTACCACCGAGTCCACGNGGTTGGGCGGTCTCCTCGGCCAA
CCAGGCGTGAACCCGGCGGATCCGAATGCAGCAAGACCCGTGGGC (SEQ ID NO. 578)

Clone Rv44

:Rv44-2ndSP6.seq:::

CCATTGGTCGGTGTGCGCATACCANTACNACGCGCGGGCACCTGACGCGGCGGCGCAACCATTCGGTGGCCATCGC
CATCGTCTGCCACCCGGTCAACGGACGCACCTTCTCCTGGCCGACCTAGTGCGCCACCCGCCGCGGTTGCTGCCAT
CGATCCGGTCAACATGAGCAGCGCCAACACCGAGCGGTACATGACATCTGCTGTGGAACCAAGTGACANATTCCGCCCG
CCATGATGATCNTCGACCGTCTCCGGATTCCGGT (SEQ ID NO. 579)

:Rv44-2ndT7.seq:::

GCCGGCCTGGTCAAAGGGGCGTCCGAAGGANCCGGGCTGGGTAAACAAGTTCTGGCTCATATCCGCGAATGCGACGCC
ATTTGTGAGGTGGTGCGGGTGTTGTCGACGACNACGTGACTCATGTACCGGACGGGTGATCCCCAGTCCGACATT
GAGGTGTCGAGACCGAGCTGATCCTGGCAGATCTGCAACCTTGAGCGGGCCACGGCCGGCTGGAGAANGAAGCN
CGCACCAACAAGGCGCGCAAGCCGGTCTACGACCCGGC (SEQ ID NO. 580)

Clone Rv45

:Rv45SP6.seq:::

GATCCACTGACCAGATGACATATCGAAATGCTCGACGATTCCGATGGCGATCAAGGCCACGATGCCCTGGCCGTGG
GCGGTATCTGGTGGATGGTGTACCCGCGGTAGGTTCCCGTGATCGTGTGACCCAGTCCACGCGATGGGCGGCGAGGT
CGTCGGCAGCATACCCCGCGTNTGCCGCCGAGTGCGCCTCGAGTTTGGCGGCCAGCTCTCCCCGGTAGAACTCTC
ACCGTTGGTCGCCGCGATCTTCTCTANCGTCGCCGCGTGGTCAGGAAAGGTAAACAGCTACCCGGGTTTCGGCGCTCG
TCCGCCGGGCATGAACGCATCTGCGAATCCGGGCTGGGATGCGAACAACGGACCTGTGCCG

(SEQ ID NO. 581)

:Rv45T7.seq:::

TCTACTGCCGAATCGGGGAACGGTCTCGCCACCNGGTTGTTGCGGGAATTACTCAGGACACCGAAACGTCGAG
AACTACGAGCGGAGTTGGACANAATACCGTCCCGGTTGGGCGCCCCCATCGANTTGGGAAGCNGAAATGTGCTCTGG
ACCCACCCAAGAATGACATTGCCGGCCGCCCTCCAACGGAATAGAAACNGTGATACCCGCCGCGTCTTGGAAG

GAATGGCATGCCCTGGGCGGGCGTTCCCTCCGCTGCCGGACTCCTCCCACCAATTACCGCCGAAGGCGTCCCGTCT
GC (SEQ ID NO. 582)

Clone Rv46

.....Rv46SP6.seq:.....
ATACTCAAGCTTCTGTCAACGAAATCCCGCATGGGATAACGGGTTTAGATTTGACAACGGGACCGTGTCTCAACA
AGCCGGTCATCAGCTGGGCGGGCGACAACGGTATCTACTTCACCCGCTTTCGCCCGT (SEQ ID NO. 583)

.....Rv46T7.seq:.....
CTGGCTCAAGCGCTCGGCGCGCAGGTGAACCTCGGACCGGCTCGACGTCGCCGAACGCGAGGCGGTGCTGGCCACGCC
GACGCCGTCGTGCGACATATCGGCACCGTGCACAAGTCTACAACAACGCCGGCATCGCGTACAACGGCAACGTCGACA
AGTCGGAATTCAAGGACATCGAGCGCATCATCGACGTCGACTTCTGGGCGTCTCCACGGGCCC
(SEQ ID NO. 584)

Clone Rv47

.....Rv47SP6.seq:.....
CCGCCCTCCGCATTATGGGTCAAGAACCATCGGGTCGGACTTCTGGGCTTCCAACGCTCGCGCCGTCCCN
(SEQ ID NO. 585)

.....Rv47T7.seq:.....
CCGTGGCACTGTGACACATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCGCCGGCGGTGATGGCGTCACC
CTACCCAAGCCGAACGCGGAAACGAGAACGTGTTCCATTATTAGGGTGTGAGCACAATACCAGATTGCTCACCAGGAA
CTCAGCGAGCACCGGGACGGATGTGCGCCACACGCCCATCTGGGTGGTAGCGGGGAAATACCGTAACCGCGGCTCC
GGTGCCG (SEQ ID NO. 586)

Clone Rv48

.....Rv48SP6.seq:.....
TACTCAAGCTTGTCAAATATCGAAGCGTCGGGTCCGAGGCTCGGTCCGCAGCTCCAGCAAAACCGCTCCACCCCT
AGATGCCGGTATCCCTCAAGGTCTTTATCCGCGCTTCACCCCACTGGCACACGGTCACCGGCACGTGCCCCCGGCC
ATGGCGCGCAACCGCTGAAGCGGACCCGACAGCCGCTGCGGTGATGGACTGATCGCGATCCACCGGCATTGAGCCGG
GCTATCCGCGGGGAAGTTCGCCGCTCCCCCGCCACATACAGCGGAGGATAGGGCTTTGTACCGGCTTCGGCCAGCAG
TAGATCGGATCGAAGTCCACATATGTCCCATGGAATTCGCCCTGCTCCTGCGTTGAGATCTCGATTATCGCGCGCAAC
CGCTCATCGATCACACGTCCGCGCACCGCAGGCTCCACACCATGGTTGGCGACTTCTTCGCGCAACCAGCCACACCCA
CGCCGAAACGAAACCGTCCCTGCG (SEQ ID NO 587)

.....Rv48T7.seq:.....
CAGGCATGCAAGCTTGGCCAACCTCATCGGACTTGAAGGTGCCGTCTCGTTGGCGGCCCTGCTCCACGGCACGTT
GATGGCACCAAGGAATGTGTCCGGGCGCTGGCTTTGTTCTGCGGCAGGTGCGCGGGGGCCAGGATCTTGCCGGAGAA
CTCGTCGGGAGAGCGCACGTGATGAGGTTCTTGACGTTGATGGCCGCCAGGACCTCGTCGCGGAATGCCGAATCGT
GTTATCCGGCGGGGANGCGGTGTAGGAAGTACCGGCCGGCTGACCGGCTCGCTGGACAGCGGGCGTCCGTGAGCTC
C (SEQ ID NO. 588)

Clone Rv49

.....Rv49SP6.seq:.....
ATACTCAAGCTTCAAAACAGGCCTGTTGTGGGCGCACCCGGCTCGCCGAGTTCTGCACGCACCGCCTCAAGTGCGGCC
CGCACCGCCGGCATCTCCCGGTACGCAGGGCCGCGGCCGCGCCGACGCGCGGTGTTGCGCGAGTTGCGCGTCA
ATGATGCTGACCTGATCGGCCACCCGGGCGGTCTCGGCGTCTGCTCCGTTCACTAATCGCGGTGCTCAGCAGCGTCTCG
ACAGCCACCACCGAGTGGAGACCAGATGCNCCACCACGGACCGCAGCGATGCCAGTCACCTCACCCTGCTC
(SEQ ID NO. 589)

.....Rv49T7.seq:.....
CAGGCATGCAAGCTTTGCAAGTTGCTGAGTAATGTCCGCCAACGTCACCACAATCGCGATGAATCAATCATGCCGCC
AGGGCGGCCAACCAATGGTGGCCGCGAGCGGCAGCTCGATCGCAGCGCGGAGGTTGCCGGCCGCGAGTTGATTACG
AACAGGGTGAGGTATAGGCGGGCAGGATAGTGACGAAGGCAAGACCTAGATCTGCCGTGCGAAGAAGAATCGAGTAT
CCGGTCGACACAACGGAAGCGAAAGTGTCCGCGATGTTGATGAGCGTCGCCGTTGTGGCGGGCGGTGGCGGGCGGTAGC
ACCGTCCGCACATACCGCGGAACCGCGGCATCCGAATTTGGGGCAGGCTGTTCAAGGCGGCTGGCAACTCACCATGA
ATCT (SEQ ID NO. 590)

Clone Rv4

.....Rv4SP6.seq:.....
CCGGCTCGTATGTTGTGTGGAATTGTGACCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCCAAG
CTATTTAGGTGACACTATAGAATACTCAAGCTTGGCCGCGAGGGCCGAGTCGATTGGTCGCGGTGCGCTCGACAGTTAG
CTTATGCAATGCTAACTTCGGGGCAAAGTTTCAGGCGGATCGGCCGATGGCGGGCGTAGGTGAAGGAGACAGCGGAGGC
GTGGAGCGTGATGACATTGGCATGGTGGCCGCTTCCCCCGTCGCGTCTCGGGTAAATGGCAAGGTAGACGCTGACGTC
GTCGGTCGATTTGCCACCTGCTGCCGTGCCCTGGGCATCGCGGTTTACCAGCGTAAACGTCGCCCGGACCTGGCTGCC
CCCCGGTCTGGTTTCGCCGCGCTGACCCGCGTCGCCCATGACAGTGCGACCCTGNACCGGGCTGGCC

(SEQ ID NO. 591)

.....Rv4T7.seq:.....
GTGTGCTGTCAATTCAGAGCTGAGCCTGATGCACTCAACTTACTGAGCATGCTAACGCTGGTCGTGCGGGTCTTGTTTC
CCGCGTGTGCGGCAGGGCACACGCTCGGGGCGTAGCTGGGAGAGGCCCGGTCAAGCCCGGAGAGCAGTGCTCAGTCCG
CCAGCTTGACCGACTTTCGATGAGAACGCGCTTCTCGCCGTATTGAACTGGCGTGCTGACGGTCGCTGAGCAGCGCTC
GCCGAGTGCGGCCGCTGATTCTTTCATCGAGCCAGGAGGCGCATTCTGTGTCGGCCGCTGCGGGTGGCCCCATCGT
CGACGCGATCCGTCACCCACTCCTCGATCAGGTCTGCCTCATCGAACGGGCCAACGGTGCTGTGCGAGTAAGTGTGCG
TGGGCACGCGAGCCGGGTGCTGTGGTACACCCACCGTTGCATGAACAA

(SEQ ID NO. 592)

Clone Rv50

.....Rv50SP6.seq:.....
ATACTCAAGCTTCACCAGGCGCCGGCGGGCCGCGGCCAAGCCAGGCAGCCGCGCTCGGCGCGTTCGGGGCCTTCCGC
CGGCTCGGCCGACAGTTCGATCTCTGGATCGGCGGGGCTCTCCGGGCCGCTCGGCGACCTCAGCGGGCCGCGCCTT
CCGGCCGAACCATTCCTAGCCATAGATAACCGCACCTCAATGCACGGTTTGGCGGCAACCCGG

(SEQ ID NO. 593)

.....Rv50T7.seq:.....
AGCTTCCGTACGACCCGCCCTCGCCGGTGCCGGCGCCATCGGTCATCGGATCTCATGACGACGTACGTAAGGCCCGC
TAGCCGCGAGCGGGCGCGGTCAACTGGCGAGGCGGGCGGCGACGTGACTGAGCTGGCCGAGCTGGACCGGTTACCCGC
GAACTACCGTTCTCGCTCGACGACTTTCAGCAGCGGGCTTGACGCGCGCTGGAACGCGGCCACGGTGTTGCTGGTGTG
CGCGCCGACCGGCGCTGGCAAGACGGTGCTG

(SEQ ID NO. 594)

Clone Rv51

.....Rv51SP6.seq:.....
ATACTCAAGCTTGCCGGGACCGCGGAACAGAACCGGCGGTTCTTACCGCGGTGTGCGGCCGGCGCGATATCGGCCTCC
CGACTAACCGAACCCGATGTGGGCTCC

(SEQ ID NO. 595)

.....Rv51T7.seq:.....
ACGTTGGCTCTGCCGAACGTATTTCCAGCGGCACGCATTGCGCGTGGGTGCCGGGCGCCGAGTTGCGTCGCTGGGAT
CACGCAGCAGTCGCCGGCGGCTGCCGTGCGGCTATGAATTGCACCGAGCCGGAATCCNCAC

(SEQ ID NO. 596)

Clone Rv52

.....Rv52SP6.seq:.....
ATACTCAAGCTTGTGCTATTCCGTGGCACTGTGAGACATATGCCCGCTCCTCCTCATCGCTGCGCTCGGCATCGTCG
CCGGCGGTACGGCGTCAACCTACCCAAGCCGAACGCGAAACGAGAAGCTGTTCCATTATTAGGGTGTGAGCACC
ACCAGATTGCTCACCAGGAACCTCACGCAGCACCGGGACGGATGTGAGCCACCACCCCATCTGGGGTGGTAGCGGGGA

(SEQ ID NO. 597)

.....Rv52T7.seq:.....
CGTTGGTAGCCCGATATGCATAGTGTATCTTACTGAACATGATTTCATTATGGAGCCCGGGGTGCCGGCAGCGCGAA
CGGTGCGCCGTGACGCGGGGCGGCACTGACCAGGGTGTGCGGGCGAACATCGGCCCGGCTTCGGATTCCGGTCCGG
GTACCGGGCGACCCACCGCTTCGAGGTA

(SEQ ID NO. 598)

Clone Rv53

.....Rv53SP6.seq:.....
ATACTCAAGCTTGGCCAACTCCTCATCGGACTTGAAGGTGCCGTCTCGTTGGCGGGCCCTGCTCCACGGCAGTTGAT
GGCACCAGGAATGTGTCCGGGCGGCTGGCTTTGTTCTGCGGCAGGTGCGCGGGGCCATGATCTTGCCGGAACCTC
GTCGGGAGAGCGCACGTGATGAGGTTCTTGACGTTGATGGCGGCCAGGACCTCGTCGCGGAATGCCGAATCGTGT
ATCCGGCGGGGAGGCGGTGATGAGGTACCGCGCGGCTGACCGGGTCTGACAGCGGGCGTCCGTCCAGTCCCA
CTTCTTGCGGGCGCGCTCCAACNACTTGACTTCTCCTGG

(SEQ ID NO. 599)

.....Rv53T7.seq:.....

600
 ATATCTTAAGCGTCGGGTCCCGAGGCTCGGTTCGGCAGCTCCAGCAAAACCCGCTCCACCCCTAGATGCCGGTATCCCT
 CAAGGTCTTTAGCCGCCGCTTCACCCCACTGGCACACGGTCACCGGCACGTGCCCCCGGCCATGGCGCGCAACCGCT
 GAAGCGGACCCGACAGCCGCTGCGGTGATGGACTGATCGCGATCCACCCGGCATTGAGCCGGGCTATCCGCGGGAAGT
 TCGCCGGTCCCCCGCCACATACAGCGGAGGATAGGGCTTTGTACCCGGCTTCGGCCAGCAGTAGATCGGATCGAAGT
 CCACATATGTCCCATGGAATTCGCTGCTCCTGCGTCCAGATCTCGATTATCGCGCGCAACCCGCTCATCGATCACAC
 GTCCGCGCACCGCAGGTCACACCATGGTTGGCGACTTCTTCGCGCA (SEQ ID NO. 600)

Clone Rv54

.....Rv54SP6.seq:.....

ATACTCAAGCTTGTGCGGTAAACCCGAGCAGGGCGGTGGGTGCGGTGTCAAAAACAACCACACTTCTTTGCGGTTC
 GGTGATCTCGACACCGGCCGCGAGCCGACCACCATGCGCGCGTAAATCGGCGATCAGCGCGTCGGCTATCGCCTGGGT
 GCCGCCACCGGAATCGGCCAGCCGACCGAATGGGCCAGCGTTGCCAGCATCAGTCCGGCGCCGGCCGACACCACTGA
 CGGCAACGGTGAAATCGCGTGGGCGGCAACGCCGGTGAACAACGCGCGGGCATCTCGCCGCCAGCGACCGCCAGGC
 AGGGGTGCCCTGGGCCAGCATCCGCGAGCCGAGACGCGAGCCAGTGCAGTAGGCAAGACCGCTTGTCCGA
 GACATGAACTCCACGACCGT (SEQ ID NO. 601)

.....Rv54T7.seq:.....

AGCTTATTGAACCGCGGTGCGAGGCAAGTGGACCTCATAACGACTCGGGTCCAGCGACCGCGCCAACACGAACGGC
 CGGACGACGTGGGCCAGGGTCGCGGCCCTCCCTACAAACAGGATCCGTTGCCTGCGAGCGACAGGCTCCGGTGCGGCG
 TTGGGCGCCGTGCTCGTCCAGCGTCCGGTCCCGGGTCGCGGCGACGCTTGTTTCTCCATACTCGCCCCCTAATCT
 CGAGGCAGCCCGTACCCGCGAGCAACCTCCCAAAATGCAATCCCCAAAATGCAATGCGTCGAGCTATTTCTCACAC
 CGACCGCTAGTTGCGGATCAGAAATCCGTTGGGCGGAAAGTCCAGCCGAATTTGTTCTCCCGCTCCGCATCATGCTT
 GTAATCGTTTGGAATTCATCCTCATATGCCTCGATCGCTTCATAGGGTCCAGGCCAAACCGGGCA
 (SEQ ID NO. 602)

Clone Rv55

.....Rv55SP6.seq:.....

CTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGCC
 AAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCCACCTCGCGGTGTGTGGTGAACCCATCTGAGCAGTGTG
 CCAAACCGGGCAGACAGCTCCCAATTGACGTGAGCCCGCTCACTTGCTGGGTAAGCGTCG (SEQ ID NO. 603)

.....Rv55T7.seq:.....

TAGCGCCCCCTCCCGGGCGGAGCTCCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGC
 CCGGCTTGATGTCGGCGTTAGCGCCGGATTCCACCACATCCCCTTGCGAAAGTCCGTTGGGTGCAATGATGAGCGCT
 TCTCCCATCGAGATAGTGGAGCAACGCAATCCGTGCGGTACGGTTCGCGTCTGATGTCGCGACCTTGGCGT
 TGACACCATCTTTGTCATTGCGGCGAAAGTGCATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGG
 TAATCCGGCCATGCGCGTTGCGTCCACCGCGACCGTGCAGCGGGCGCACACGCGACTTCTCCGGGGTTGACCGGGTGA
 TCTCGGCGAAATCAGATACGCTGGCGCCGCGACGACCAAGCGTCTGGGCTTGTTCTTGCGAATTGCATGTCTAATCA
 GGTCTTTCTC (SEQ ID NO. 604)

Clone Rv56

.....Rv56SP6.seq:.....

TGAAACTATATAATACTCAAGCTTGCCAAAGAACCTCGTCGACCAAGCAGGACGCGACCGTCGAGGTGGCGATCCG
 GCTTGGCGTCGACCCGCGTAAGGCAAACCAGATGGTTGCGGGCACGGTCAACCTGCCACACGGCACTGGTAAGACTGC
 CCGCGTCGCGGTATTGCGGTTGGTGAAAAGGCCGATGCTGCCGTTGCGCGGGGGCGGATGTTGTCGGGAGTGACGA
 TCTGATCGAAAGGATTACAGGCGGGCTGGCTGGAATTCGATGCCGCGATCGCGACACCGGATCAGATGGCCAAAGTCGG
 TCGCATCGCTCGGGTGTGGGTCCGCGCGGCCCTGATGCCCAACCCGAAAACCGGCACCGTCACCGCCGACGTCGCCAA
 GGCGTTCGCGGACATCAAGGGCGGCAAGATCAACTCCGGGTTGACAAGCAGGCCAACCTGCACTTCTC
 (SEQ ID NO. 605)

.....Rv56T7.seq:.....

GCTGAGCTCCACGGCGTGGATCAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGATGTCGGC
 GTTAGCGCCGGATTCCACCACATCCCCTTGCGAAAGTCCGTTGGGTGCAATGATGAGCGCTTCTCCCATCGAGATA
 GTGGAGCAACGCAATCCGTGCGGTACGGTTCCGGTTCGACTCGATGTCGCGACCTTGGCGTTGACACCATCTTTGTC
 ATTGCGGGCAAGTGCATCATCCGGTAAGCGCGCTTATGACCGCCGCTTTGTGCCGGGTGGTAATCCGGCCATGCGC
 GTTGCGTCCACCGCGACCGTGCAGCGGGCGCACGCGACTTCTCCGGGTTGACCGGGTGCATCTCGGCGAAATCAGA
 TACGCTGGCGCCGCGACGACGAGCGCTGTTGGCTTGACTTGCGAATTGCCATGTCTAATCAGGTCTTTCTCT
 (SEQ ID NO. 606)

Clone Rv57

.....Rv57SP6.seq:.....
ATACTCAAGCTTGTGGTGACCTCGCCGGCGAACAGTTCTCGCACGATTTCGGGATTAGCGGGACTGGTCACCAAGTTG
GGTATGCGGGAAGGCGCTGACGTTCCGCCGCGATTAGCTGTTTGATGGACGCGGCGGTGATGTCCTGATCACGGAAGTG
GCTGTAATAGCCAGGGTCGCCACGCTTCCATCCGGGCCCGGACCCGGC (SEQ ID NO. 607)

.....Rv57T7.seq:.....
GATGATCGCCGGTGCCACCCGATCCGTGCCTCGGTACGCGGAACGTGCTTCCGGTCCGGCGACCACCATGTCGCA
CGCACCGACAGGCCGAACCCGCCGCCGACATGCCGTTGATGGCGCCGACCACCGGCAGCGGCGACTCGACGAT
GGCGCGCAACAGCGCCGTCAATTCGCCGCGCCGCGCCACCGCCATCCGGTACGGATCACCACCACCTCCGCCGGCCTC
GCTGAGGTCC (SEQ ID NO. 608)

Clone Rv58

.....Rv58SP6.seq:.....
ATACTCAAGCTTGCCGCAATCGAAACCAACCTGTTTGTGCCGCAAGAAATTACGCCGTGGCCCGCGCCGATCAAGAA
ACGCCCGCGCGCGCGCGGTGTCTGTCGTATGGCATGACGGGCACCAATGTGCACGCCATTGTGAGCAGGCACCGGTG
CCAGCCCCGAATCCGGTGCACAGGCGACACCCCGGCCACACCGGTATCGACGGCGCGCTGCTGTTGCGGCTGTG
GCCAGCTCGCAGGACGCGCTGCGGCAAACCGCGCGCGGTGGCCGATTGGGTCT (SEQ ID NO. 609)

.....Rv58T7.seq:.....
TTGGCGGGTTGGCCACANCANCCGCCGGTGACGGCGACGATGCTGGGCTGGTTGCGGCCCTGCGCCACCGCGGCTTG
CATGCTGGTTGGCTGTCTTGGGACGATCCCGAAATAGTCCACGCGGATCTGGTGATTTTGGCGGCTACCCGCGATTAC
CCCGCGCGGCTCGACGAGTTTTTGGCCTGGACTACCCGCGTGCCCAATCTGCTGAACCTCGCGGCGGTTGGTGGCCTGG
AATGTCCANCGCCGTTACCTACGTGACCTTGATGGGATCCGGGGNT (SEQ ID NO. 610)

Clone Rv59

.....Rv59SP6.seq:.....
NCGTGGACACCGGTGTCGANCGCCACCAGCCGATGTCTGCANGTCNATTCCGTCCTCGGCAACATCTTGAATGCCGA
GCACGCCTGGGCGTGATCGGCAACCGGGGATGACCGCTCGCCGATCCGCTCGACAATCCCGCGGCACGTGACATGC
CGGCGGACGGCTCGACGAGCTGGAACCTCAGCGACGACGATCCGGAATTGATCACCAGCACGGTGCTACTCATGGACC
CCTGCGCCTGAATCCCGTGATGGCCACGGTGTGACTATTCTGTCGACAGTGCACCCGAGATAGTCTTCACGGCTGCGT
(SEQ ID NO. 611)

.....Rv59T7.seq:.....
CATGTATTGCCGTGCTCACGGCGCCACGCTCGATGGTTTCTCGAAGTCTCCGGGCTGGTGACAGCTTCTCGTTGATC
TCGTTGCGCCACGCCGTCTCTTCCCGCCGACGACCCGATCTCGATCTCCANAATGATCTTGGCGGCCGCGCCGCTT
GAGCAGCTCCTGGGCGATGGCCAGGTTCTCATCGATGGGCACTGCCGACCGTCCACATGTGCGACGGAACAAAGATG
TCACCTTGCTCACGCGTGCNAGATCNCANAAGGGCCGGACATACTGTCNACTTGTCTTGGGCACTGGTCCGTGTC
AGCCACGTGACGGGTACTTGGCGGATAACGTGGTG (SEQ ID NO. 612)

Clone Rv5

.....Rv5SP6.seq:.....
GCCACCAGACCCGGCGTAACCTCTGCTCACGGAAATGCGGCCAGGCCGCGCGTAGCACGTGGTATCCGCCATAAAGG
TGACCTTAAGCACGGCGTCCCAATTCTCGAACGACATCTTGTTGAAGGTGCCGTGCGGCAAGATCCCGGCGTTGCTC
ACCACACCGTGACGGCGCCGAATTCGTCAAGCGCGGTCTTGATGATGTTGCTGCGCCGTCTCGGTGGCGACGCTG
TCCTTAGTTGGCGACCGCCCGCCCCCTTGTCGCGAATCTCGGCGACGACCTCATCGGCCATCGCCGAACGGCGCCC
GTGCCGTGCGGGGCGCCACCGAGGTGCTTGACCACGA (SEQ ID NO. 613)

.....Rv5T7.seq:.....
CAGGCATGCAACCTTTGTCCACACGCGTCTACTCCGTGCAAGGTCCGACCGCTTCCACGTCCCGCGGTGACGGTGCT
CCATCTCCCTCAGCAACGCGTGAAGTGGTCCGATCCCGCGGCTTCAGG (SEQ ID NO. 614)

Clone Rv60

.....Rv60SP6.seq:.....
GTTGAGACGCAACCAGCGCACAAACGACGATTTGGCGTAGCGGCGGACGTCTGCTCGATTTCGATCACGTGCGGCTCGCA
TCGAGACTGGCCCCGCGACGCTACACGATCGCCGTGCTCGATGACACGACCGAGCCGTACGCCGGCCGTAAGCCGCGCC
AGGATTGCGGCGAAAAACGTCTACGTGGCGGGTGTACTGGGTGTCGAATGATTCTGGGGTGCGTATGCGTCCTGCAAT
CGTCGACATAGATCCGTGCGCGCATCGCGTCGACAACCTCCGGTGAGTGGAATACACTTGCCGATCACGCGACGTGCG

CGGATCGATGCCGACCGAAATACGACCACATGGCTCTTGTTCNCAGTGTTGGCGGCATCAAATACCCTCAGTGCCGT
CCGAC (SEQ ID NO. 615)

.....Rv60T7.seq:.....
TTNCCGCCTTNACGCCTACTCCNAGACGATGCTCGACGCGTGTGAGCACACGGCGCTGCTGTAGACGGCACGGCGCAG
CTGGATCGCGCTTGGTGCACCAAGCCTCTACGCGCGTTCGCTGCGTTCATCGGGTACCGAACATATTCGGTTCGTT
GCGCAGAGTGTGCATGTGCGGCTCTTGTGAACGAACATAGCAAAGCGTATATGTCTGTGGCGGCTCTGCAGATATCGC
GATAATACGTATATACATAAGGTGGCGCGCATCTATCGGTATATCCGTTATGGCGGACGTGCGTGAGCGTGAGTCCG
GGCGCATCGCGCACTTCGCGATCGCGTGACTGGTCTCGCGACTGCGCGCATGCGTAGC

(SEQ ID NO. 616)

Clone Rv61

.....Rv61SP6.seq:.....
GGTGATGACGCACTTGCTTCGAATGAGTCATTGACTACTCCCGTGGTTGTCTGCGATGGTGGAGTGCCGCGCAGCCT
TGCCCCGANGTTCGCGATCGCGTTCGCGGGCTTCGGGGAGCAGACTGACCTGCAGATGGAAGTCGTGCCACATGCCCGCGA
ACGGCGAGCTCGATGCTTGTTCGAAGNGCGCANGCGGTTTCGATCTTGTCCGCGTCAACGCAGATCGGATCTCGCC
GCGGTCTGCATGACGATGGGCGCAGGCCCGCTCATGTCCCGTAGACGGGGAGATACGGGCAGCCGCGGATCGAGACCT
ACGTAGCGCGGCGCCCATCGTGCCATCGACGAAGATGACGGATCGCGCAGCGCCGTTCGCGTTCGATGTACGC
GAGATCGCCACGGCAGATCAGCGATGCGCGGGC (SEQ ID NO. 617)

.....Rv61T7.seq:.....
CGGTACGCCGGCAACAAACGCCTTGTGACGAGCGCTCCGAGCGGTTCATCGGCCTCCACCGTCATGCACAGCTCCTTC
TCCAGGTCTACGCCGACGTTCGCGGTCCACATTGGTGAGCTTGGCGAATGCCTCGGCAACCTCGTCGAAATGCGCCTCC
GCGTCCGCATCGAAGGTTCGCCATGTCAAAGATCAACTCGACGTAGTAGCTAGTTACCGCATCAGGTGAGTGTTCGCTG
GCCTCGGAGTCCGGCCGAACAATGGCCATTTCCCGGACTCTAGAATCCAGTCATCGTCTCGGTGACGACGCCTTGCC
GATCACATAGCTCGACCGGATCGGAGAGAATCTGGTTCTCGT (SEQ ID NO. 618)

Clone Rv62

.....Rv62SP6.seq:.....
ATACTCAAGCTTAAGCGCAGCAGTACCGGCGGTGCCTGGGCATCCAGCAAAACGGGGAGCTCAACGAACGATTTCCTG
AACGAAGGGTCGTCCACCAACCTCAAACCGAACGGTTGCCAGCCCCGGC (SEQ ID NO. 619)

.....Rv62T7.seq:.....
GCAAGTCCGCTCAATGTGGTTGTGATCACANGACTACGTCGCCTCAATCAGCTCAAACGTCACCCCGTGGCGTGCTGC
GCAGCATGAAGGTTCGGCGCCCGCAGATGTGGGCGAAGCAACAGGTAATAACTGGTTCGGCATGGGTCAACCCTCATTG
GGCCGTTGCGGATCGGGTGCACGCCCGAGTGCCGGTCAACTCAACACCGCCTTCACCGATCTTTTCGTGAAAATG
GCGGTGCTGTCGGGGTATACGTCCGCGATCCACGAGGCGGAATCCGCTGAGCCGCACTGA

(SEQ ID NO. 620)

Clone Rv63

.....Rv63SP6.seq:.....
ATACTCAAGCTTCGCGCCCTCAAGCGGCTGAAGGTGGTTCCGGCGTNCCAACNGTCGGGCAACTCGCCGATGGGCATG
GTGCTCGACNCCGTCCCGGTGATCCCGCGGAGTTCGCGCCGATGGTGCAGCTCGACGGCGGCGGTTCCGCCNCGTCC
GACTTGAACGACCTGTACCGCAGGTGATCAACCGCNACNNCNGNTGAAAAGGCTGATCGATCTGGGTGCGCCGGAA
ATCATCGTCAACAACNAGAANCAGGATGCTGCNGGAATCCGTGGACGCGCTGTTGACAATGGCCGCCGCGCGCCGCC
GTCACCGGGCGGGCAACCGTCCGCTCAAGTCGCTTTCCGATCTGCTCA (SEQ ID NO. 621)

.....Rv63T7.seq:.....
TGCGCATGGCAGTTGTTGCCGGCTTGAGTCGCGTATAGCGGGATTCCACCACATCCCTTGCGAAGTCGTGGGTGCAAT
GATGTAGCGCTTCTCCCATCGAGATAGTGAGCAACGAATCCGTGCGTACGTTGGGTGCTACTCGAGTGCGCANCTT
GGCGTTGACACCTTTGTCAATTGCGGCGAAGTCGATCATCCGGTAAGCGCGCTTATCGACGCCGCTCTGTGCCGG
GTGGTAATCCGGCCATGCGCTTGCCTCCACCGCGACGTGCAGCGGGCGCACACCGACTTCTCCGGGTGACGGGTGATC
TCGGCGAATCAGAACCTGGCGCGCGACACAGCGTCTGGCTGTACTTG (SEQ ID NO. 622)

Clone Rv64

.....Rv64SP6.seq:.....
TGGGTGATCAGATACTGGCTAGTTGGTTCGGGTGGGGTGATCGAAGATCGCGGTGGCCGGCAGCGTTACTGCGGTGACG
CTGTAAAGCGGTTACGTACTCCACGGCACTCAANGAATTANATCCCGAATCGGCAACCCCTGGCCAGCGTCGAGTCCG
CAGCGCCGTTCGCGCCCCCACCCTGCGGCATGCTCACATACCACCTCGATCGCTGCGGGAGTTGCTCGTTCGGCCGAC
CGACCGGCCAGCCGGGCGGCAACCGGAGGACCAAGATTGAGCACCACCATCGCTAGCCCGATCTGGCCGCGCGTGG

(SEQ ID NO. 623)

.....Rv64T7.seq:.....
TCGTAGCGGTTGCGACCANTCCGCGGACAGCTCCGCCACGCGACGGGTGCGGGATCACCGCGGTCAAACCACCGAGCGG
CGAGGATCTCTGGCCGTGACGCTGACCGCGCACGGCCGCGGTGATGGCCAGTCCCGACCGCGGTTCCACTTGGCGTAC
GCGCTGGATGTGTTGTGCCGCAACGGAATCCCACTCAATTATGACCTCGTTGTGGCGAGCGCGGTATCGTACGCCC
GACCAGGAATCGTCGATGCTATCTCACGTACCGAAGGCCTCTCCAGCACACCGCATCCAGAACGTGCACACNGTCG
ACATGTCTCGGCGGATCCGCCTGCAGAACGAACGCCANGTCCGCTGTGCGACACGGGTGCGGATCACCGCTCGCACGC
GGAGATCGGCACACGCGCAGCGCATCGATCATAATCTCTCGATGCGGTCTCCACCACCGAACAG

(SEQ ID NO. 624)

Clone Rv65

.....Rv65SP6.seq:.....
ATACTCAAGCTTCGCTGAGGTGGTGGGGCACGATCACGTACCGCACCGCTGTGCGGTGGCGCTGGATGCCGGCCGGAT
CAACCACGCGTACCTGTTCTCTGGGCCGCGTGGCTGCGGAAAGACGTCGTGAGCGCGTATCCTGGCNCGGTCTGTGAA
CTGTGCGCAGGGCCCTACCGCCAACCGTGGGGGTCTGCGAATCCTGCGTTTCTGTGGCGCCCAACGCCCCGGCAG
CATCGACGTGGTAGAGCTGGATGCCGCCAGCCACGGCGGCGTGGACGACACCCGCGAGCTGCGGGACCGCGCTTCTA
TGCGCCGGTCCACTCACGGTACCGGGTATTTATCGTCGACGAGGCGCACATGGT

(SEQ ID NO. 625)

.....Rv65T7.seq:.....
GCACTCACGCTGGTACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACTTGAACCTGGTCTCGTTTCGGCAATAA
CTCGTTTCGGCGTGCAGGACGCGGCGCAAACGTAATTCGGCATCAACGCGTCCGACCTGAATTGGCAGCAAGCGGCGCT
GCTGGCCGGCATGGTGCAATCGACCAGCACGCTCAACCCGTACACCAACCCCGACGGCGCGCTGGCCCGGCGGAACGT
GGTCTCGACACCATGATCGAGAACCTTCCCGGGAGGCGGAGGCGTTGCGTGCCGCCAAGGCGATCCGCTGGGGGT
ACTGCCGACGCCAATGAGTTGCCGCGCGGCTGCATCGCGGCGGCGACCG

(SEQ ID NO. 626)

Clone Rv66

.....Rv66SP6.seq:.....
ATACTCAAGCTTGTATAAAAAGATCGGTGAGCGCATCGATTGCTCCGCCGGGTTTGCCGCTGCGGCGGCGGAGCTGC
CGTGACCGTCTATTTGGGTGATCAGATACTGGGCTAGTTGCGTCCGGGTGGGGTGATCGAAGATCGCGGTGGCCGGCA
GCGTTACTGCGGTGACGGCTGTTAAGCGGTTACGTACCTCCACGGCACTCAAGGAATTAATCCCGAATCGGCAAACG
CCTGGCCAGCGTCGAATCCGGCAGCGCGCTCGCGCCCCAGCACCGCTGCGGCATGCTCACATACCACCTCCATCGCTG
CGCGAATTGCTCGTCCGCCGACCGACCGGCCAGCCGGGCGGCAAACCCGGAAGA

(SEQ ID NO. 627)

.....Rv66T7.seq:.....
CCTCATCATATGCCGATAGAGCTTACATATTGAGGAGATCACCATGGCTCGTGCGGTGCGGGATCGACTCGGGACCAC
CAACTCCGTCGTCTCGGTTCTGGAANGTGGCGACNNGTTCGTGCTCGCCAACTCCGGAGGGCTCCAGGACCACCCGTC
AATTGTCGCGTTGCGCCGCAACGGTGAGGTGCTGGTCNGCCAGCCCGCAAGAACAGGCAGCTGACCAACGTCGATCGC
ACCGTGCGCTCGGTCAAGCGACCATGGGCAGCGACTGGTCCATAGAGATTGACGCAAGAAATACAGCCCGGAGATCT
CCCGCATTTCTGATGAACCTGAACGCGACCCGAGGCTACTCGGTGANGACATNACGACGCGTTATCACACCCCGCTNC
TTCAATGACCCACGTCNGGCACCAAGGACCCGGCAATCGCGGCTCACTTGNGCGATNGTCNACAACCAACGCGNCGC
CTGGCTACGGGCTCAACAAGGCANAAGACACAATCCGCTCTCGATTGGTG

(SEQ ID NO. 628)

Clone Rv67

.....Rv67SP6.seq:.....
ATACTCAAGCTTATCGAGGCGGCGCATACCGAAGCGTGGGAAATCCAGACCGAATACCGCGACGTGCTGGACACTTTG
GCCGGCGAGCTGCTGGAAAAGGAGACCTGCAACCGACCCGAGCTGGAAAGCATCTTCGCTGACGTGAAAAGCGGCCG
CGGCTACCATGTTGACAACCTTCGGTGGCCGGATCCGTCGGACAAACCGCCCATCAAGACACCCGGCGAGCTCGCG
ATCGAACCGGCGGAACCTTGGCCCCAGCCGTTCCCGAGCCGCGGTTCAAGGCGGCGATTGCGCATGCTACCCAAGCC
GCTGAGGCGCGCCGTTCCGACCCGGCCAAACCGGGCACGGCGCAACGGTTGCCCCGCCGCAACCGGTCCGGTGA
CCGCAGTACGGTCCCCCAGCCTGACTACCGTGCCCCGGCGGGCT

(SEQ ID NO. 629)

.....Rv67T7.seq:.....
TGGCCGGGCTGGTAGCCCGGTATGGCAAGGTTCCGCTCAATGTGGTTGTGATGCAGCAGGACTACGTTTCGCCTCAAT
CAGCTCAAACGTACCCCCGTGGCGTGCTGCGCAGCATGAAGTTCGGCGCCCGCACGATGTGGCGAAGGCAACAGGT
AAGAACCTGGTCGGCATGGGTGAGCCCTCATTGGGCCGTTGCGGATCGGGTTGACGCGCGCCGGAGTGCCGGTTCGAA
CTCAACACCGCCTTACCGATCTTTTCGTGAAAATGGCGTCTGTCCGGGGTATACGTCCGCGATTCCCACGAGGCG
GAATCCGCTGAGCCGACGTGATCCGGGCTCGCCGCGGCGTGATCCTGGCCTGTGGTGGTTTCGAGCATAACGAGCAG
ATGCGAAT

(SEQ ID NO. 630)

Clone Rv68

:::Rv68SP6.seq:::

GTCCAGTCAAGCATCGGTCTCTCCGACTACGCCAAGANTGGCGACGTGTCTAGTGCANACAGCGGANATGGTGGCGCC
TATGCGTCGACGCTCACAAACNGCGGTGANCGCGTTCTGGTCGTGCACCATCGAGCCGTGCCAGCCCGGCCGCGTGCC
GTCAGCCGCATCCACTGGATGCCTTCTCGNGTTTCAATCANGTACANGCGACGTTCCGCCACCATCGTGCCGGGGCAC
GGTTAGCGAGAAACCGCGACTTCACCGATTGCCTCGGTGATGCCGTGCAACAGATCGGGCCTATTGTGACAGCCAG
TGTGATNCGTATTTGCCGCCGTGCTCCTCGTCGCAACGATGCGAACACAGATCCGTGGNGGACGATAGCGGCTGACAA
NGTGGGGGCAACACAATCACATGCCACATTTCTTCATTTACGCCCCACAACCCAGACTTCGTCTCGATGNGCCG

(SEQ ID NO. 631)

:::Rv68T7.seq:::

CACGCGGTCTGGCCCGATCCGAAGATCCCTTTGCCGGCGTGGCGGCTCTGCTCGGCGGTGTTGTACACTTCTCGAACA
CCTCGGCACCGACACCACCACCGTNGCTTGAACACCGCCAACATCGGCAGCAGATCTTGATGGTCTGGTGAATCCCA
CGGTGACTTTGGAGTGAAGGCGCCATACTGATCGCCGCCAGCACATGAGCTAGCGGCAGGAAAACAGCAGCCGC
TCACCTTGGCAGCAGCGTCNGGTGATATGCCTGGCGCCCTTAATCTCGTGAACAGTTGGATTGGGTCAACTGGCAG
CCTTGGGTCTCCGGTGGTGCCGANGTGTANATAAGCTCCCGGTCCGTCAACGTANTGCGCAGGCGGCGGTTACTCGG
CGGGTCAACGAGCCCGCTCGTGAGCNATCAGCCTTTGGACCGAACGGGATTCTACTCCGCAGGCGGCCCTCCGAAA
TCGGCACATGTCCTTTGATCGTTCGCAACAN

(SEQ ID NO. 632)

Clone Rv69

:::Rv69T7D3.seq:::

GGCCATGTACATCGGTGGTACAGGTAAACCGCGCCGTGTGCGCGGTCTCGGAGATCAGAACGTGGTTCGAGTTGAAC
CGCGGGCTTTAGCCAGTCGCGATAATCGGCGGAAGTCGGCGCCTGCCGCCCAACTAGCGCGACTCGCCACCTAGCA
CACCATGGCGAAGGCCATGTNTCCGGCCACGCCGCCGCGGTGCATCACCAGTCATCGACTAGGAAGCTAAGCGACA
NCTTGTGCAGGTGTTTCGGGCAGTAGCTGCTCGGAAAATCGGCTGGAACCGCATCAAATGGTCCGATCGAACCG
GTTACCCGATCGTCACAAAATCTCCGTCCT

(SEQ ID NO. 633)

Clone Rv6

:::Rv6SP6.seq:::

GGGTCTACAACACCGGGTCTGACTTCTGGGCTTCCACCGCTCGCGCCGTGCGGACAAACAGCGCGGTGCAACCGACA
CTCGTTGTGATGTCCAGCTATCCTCCGGTAGGCACCCAATCGACCCTACCCGGCTATCTACCCCCGATCTCCAG
GTCGCCCGCATCCATGCGCATCCCGGTCCGGATCCC

(SEQ ID NO. 634)

:::Rv6T7.seq:::

CAGGCATGCAAGCTTGTCTGTTTCCGTGGCACTGTACAGATATGCGCCGCTCCTCCTCATCGCTGCGCTCGGCATCG
TCGCCGGCGGTTCATGGCGTCACCCTACCCAAGCCGAACGCGAAACGAGAACGTGTTCCATTATTAGGGTGTGAGCACC
AATACCAGATTGCTCACCAGGAACACGCGAGCACCAGGATGTGAGCCACACGCCCCTCTGGGGTGGTAGCGG
GGAAATACGGCTAACGCGGCTCCGGTGCCGGCAGCCAGCGCAGACCTCGGCGGCGGACACGGCTAACACGAGCAGC
CCATAGTTGTTCTTTGCCGGATGGCGGTGTTTGCTGACATATCGGGCGCGGCGCGCGCGCGCC

(SEQ ID NO. 635)

Clone Rv70

:::Rv70SP6D2.seq:::

NCTACGCTGCTGAATGTTGTGCGCCGGAGGANTCAAGACCCACGCGGTTGTACGCGGACNTGCGACATGTTCAACCG
CCGGA

(SEQ ID NO. 636)

:::Rv70T7D3.seq:::

CTAACCAACAAGCCATGGTGGTGGCGCCGTGAGAGGTGCGCGGTGCGCCACAACGGGAAGATCGCCTTGAGCGTCGC
TCGACCGCCGCTCGAGTTGGGTCTAACGAAGTACTGATGCCGATCATGTGACGTTCCGTGCGCATCAGCGTGCAG
CGCGACCCCTCGACGAGCCTCGGTGCCGCCGCGGCCAGGGCACCAGCTGTTTTAGCGCATTGTGCTCCGCCGGTAAT
AAAGGANGTCCGTGCGCTCCGCTGCTGTGGTTGCGGAATAACATCTCCCTTCTGCAACAGGATGAGAATGGTTTTA
ATTGCTC

(SEQ ID NO. 637)

Clone Rv71

:::Rv71SP6.seq:::

CTAAGCTTTCCGGTCCGCCGCCACTAGTACCGGTTGCCGGCCCCGCCGACCTAGAATGTTCCGCCCATTGCCGTTTC
CTCCGCCGCCGGGT

(SEQ ID NO. 638)

.....Rv71T7.seq:.....
TCTGGTGCCGGGTGTGCCGACGGGTCCGTCCGCCTCTGCTTCAGTGATTCTGTGATGCGACCGGCAACGTCCTCGTTG
TTCGGTGTCTATGTGGTCCGTCTCTCCTTGTTCGCATACGATT (SEQ ID NO. 639)

Clone Rv72

.....Rv72SP6D2.seq:.....
GCGATCGNTNACCACAAGGGCGCAACCGTTCCGCGCTCGACTGAACGTGCTGCCGCCTGGAGAACTGGCGCTGCTGCC
ACCTGGTCGGCGCATCGGCACTTCGAGGACTGGATTTCGACGCGTGGCCCGACCTGANGTNGCGGTGGACNNGTGTG
CACCCGGTTGATTCCTCGGCCTTGCCGGGATGCCACCTGCGCCTGGTGGTTCGAT (SEQ ID NO. 640)

.....Rv72T7D3.seq:.....
CGTGACCGGACGGGGTGCCGCGCAACCGTCTTGCCCAATTGCCGGGACTGGGGCTGGAGTATAAAGCGGGCCTGT
TGCCGGAAAGATAAAGTCAAAGCGGTGACCGAGCTGAATCAACATGCGCCGTGGCGATGGTGGTGACGGTATTAACG
ACCGCCAGCGATGAAAGCTGCCGCCATCGGGATTGCAATGGGTAGCGGCACAGACTGGCGCTGGAAACCGCCGACGCA
CATTAACCATAAACACCTGCGCGGCTGGTGCAATGATTGAACTGGCACGNCCACTCACGCCAATATCCGCCAGAACA
TCACTATTGCGCTGGG (SEQ ID NO. 641)

Clone Rv73

.....Rv73SP6.seq:.....
ATACTCAAGCTTCTTACCCANAGCATGAACCCCGCCGTCCAATGCCGCCACCGTGGTGTGTCGGCCGGCCGGGTGCG
GGCACAATCGCCGAGTTCGCGCAACAGATCCTCGAAGGTCTTCACGGCCAGCGATTGTTGCACGTGTACGCCAGCCAA
GTCACGGTGGTTTTGACGCCACACGTTCCGCCACCGCCGCGCCGCGCATTAGGGCATCCTAATATAGGTAGGCTACCC
ANTTATTCTGTGGTCNAAGGAGGCGAGCCGAACGTGACCTTCCCGATGTGGTTCGCAGTTCGCCCGGAAGTGCCGTCA
GCATGGCTGTCCACCGGCATGGGCCCCGGTCCGCTGCTGGCCGCGGCCAGGGCGTGGCACGCGCTGGCCGCGCAATAC
ACCGAAATTGCAACGGAACCTCGCAAGCGTGCTCGCTGCGGTGAGGCAACTCGTGGCAGGGGCCAGCGCCGACGGTT
CGTCNTCCCCATCAACCGTTCCGTATTGGCTAACCACCTGCACGGTGGCACCGCACAAACGCCGCCACAAACGCGCCCC
GGTATAC (SEQ ID NO. 642)

.....Rv73T7.seq:.....
GGCCGAACTTAATCGGTTGTTGGCGGCTGCCGAGTTGGGTCACTCGGGGGGTGTGCACTGGCACATGGTGGGCCGGAT
TCAACGCAACAAAGCCGGTTCGCTGGCTCGCTGGGCGCACACCGCTCACTCGGTGGACAGCTCGCGGTTGGTGACCGC
GCTGGATCGGGCGGTTGTTGCGGCGCTGGCCGAACACCGTCTGGCGAGCGGCTGCGGGTTTACGTCCAGGTGAGCCT
CGACGGTGACGGATCCCGGGGCGGCGTCGACAGCACGACGCCCGGCGCCGTAGACCGGATTTGCGCGCAGGTGACAGGA
GTCAGAGGGCCTCGAACTGGTGGGTTGATGGGCATTCCGCCGCTGGATTGGGACCCGACGAAGCCTTTGACCGGCTG
CAATCGGAGCACAACCGGTGCGTGCGATGTTCCCGCACGCGATCGGTCTGTGCGGGCATGTCCAACAACTTGAAT
CCCGTCAACATGGTGCAC (SEQ ID NO. 643)

Clone Rv74

.....Rv74SP6.seq:.....
GCTTCCCTGATACTCGACCAGCCCCACTCGGGCCAATACGTGAATGTCCTAGCATTTTTACCCGTTACGGGCTAG
TCGAGTAGTAGACGATTGATTAGCCTGAACGTACCTCCGACGGCCAGCTGACGAACGGGTTTGACGGA
(SEQ ID NO. 644)

.....Rv74T7D3.seq:.....
TCAGCTGTCTGTAGAAGGGCTGGCGATACTGTGCACTGTCTGATATCGCNCNGTNGTGGGACTATNCAGNCCATNANG
ATGCGGTTTCNGNNNTGCAGAGNATCCTGGNACACATNCGGTTCACGTTAATCANCATCGCGANTTNCNTNCTNTTCG
ATTANTTCTGCTAACGNNTCTNNNAGTGCCGTGCGGGTCGACTCTAGAG (SEQ ID NO. 645)

Clone Rv75

.....Rv75SP6D2.seq:.....
NCTCTGCCGGGCGNAGAGCGCAGAGTCGGACGGCTTCGTGATCGTGAAGCGACCNTGCGATGANCAGATATCGNTNAC
ACTGCTCANAACTTCGGATCATCGNTGATACACAGGCCAACGGGTAGCGGTTGTCCAACCGCTTCGTCAACGANATG
GGATCGTGACGANCTACGCTCGCAGGATATGTCCNGACCNNGTCTAGANAN (SEQ ID NO. 646)

.....Rv75T7D3.seq:.....
CACTTCATGCTCGTGCGTTGGCNTCGATTTGCNCGAGNGGTTAGCTCCTCGAGTGNGTGACGTATCACTCCGGCNGAC
TANCCGTATCNGCGTCCCGCACCGGTCAACTGGTCTAGCCACACCGGGGAGAATNCNCGACCGGNGCTATCGACCNAT
CACGGCTTGTGNNAAAGATAGNCAGCC (SEQ ID NO. 647)

Clone Rv76

.....Rv76SP6.seq:.....
ATACTCAAGCTTGCCAACCGCCACCCTGCATCCGGGGGGCGAGCACTGCTCCGCCGACCAGTACGAACCAACCTGCGG
TGCCAGGCCATTGACAATGTGCTGGTCCGGCGCCCGCAGTTCTAGCACAGCAACGCCCGGCCACCACAGGGGCG

(SEQ ID NO. 648)

.....Rv76T7.seq:.....
CGGTGCGGTGTGCTTGGCGGCGTGGTATCAACACCGCCACGAAATGGGGCACAAGAAGGATTGCTGGAGCGGTGGC
TGTCCAAGATCACCTCGCCAGACCTGTACGGGCACTTCTACATCGAGCACAACCGTGGCCATCACGTCCGGGTGT
CCACACCGGAAGACCCGGCGTCCGGCGGGTTCGGCAAACTTTGTGGGATTTCCCGCCCCC

(SEQ ID NO. 649)

Clone Rv77

.....Rv77SP6.seq:.....
AATACTCAAGCTTCGCGGAGGTGGTGGGGCAGGAGCACTCACCGCGCCGCTGTCGGTGGCGCTGGATGCCGGCCGGA
TCAACCAAGCTACCTGTTCTCTGGGCGCGTGGTGGCGAAAGACGTGTCAGCGCGTATCCTGGCGCGGTGCTTGA
ACTGTGCGCAGGGCCCTACCGCCAACCCGTGCGGGTCTGCGAATCCTGCGTTTCGTTGGCGCCCAACCCCCCGCA
GCATCGACGTGGTAGAGCTGGATGCCGCCAGCCAGCGCGCGTGGAGCAACCCCGGAGCTGCGGGACCGCCC

(SEQ ID NO. 650)

.....Rv77T7.seq:.....
GATGGCACTCACGCTGGACAAGACCTTCACAAAATCTGAAATCCTGACCCGATACTTGAACCTGGTCTCGTTGCGCAA
TAACTCGTTGCGGCGTGCAGGACGCGCGCAAACGTACTTCGGCATCAACGCGTCCGACCTGAAATTGGCAGCAAACCG
GCGCTGCTGGGCGGGCATGGTGCAATCCGAACAAGCACGCTCAACCCGTACCAACCCCGAAGGGCCGCTGGCCCG
GCGGAACCTTGTCTCCA (SEQ ID NO. 651)

Clone Rv78

.....Rv78SP6.seq:.....
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTCTGGGCGTCTGGTGCCC
GGCTGCGCGGTGCAGGAAGTGGATTTTACTGCCATCTCTCGCGACCCTGAGGTGGTCCAGGCTTACAACACCGACCCA
CTCGTGCAACACGGACGGGTCCGGCGGGGATTGGCGCGCGCTGCTGCANGTGGGCGAGACCATGCCGCGCGGANCA
CCGGCATTGACCGCGCCGCTGCTAGTGCTGCACGGCACCGATGACCGGCTGATCCCCATCGAAGGCAGCCGTGCGCTG
GTCNAATGNTNGGATCNGCCGACGTGCANCTGAANGANTATCCCCGGCTGTNCCACNAGGTGTTCAACGAACCGGAN
CGCAACCAAGTG (SEQ ID NO. 652)

.....Rv78T7.seq:.....
CAAGGCATACGCCAAGACCCAAGGATCGCAGTCACCTCCGTCAACGGCCTGGTCCGCCGCCACGGGTCCGTGCAGGA
GACGTGGCTGGCCATGCAAAGCGCCGCCGCTTATCAGGAACGCCCCGGCTTGTGCGCTTTCTGCATCGACACATT
TCCGGAGGTGTTGTGGTTGGCGCANCGCGGAGACAGGCCTGGGATGGCGTGCATCGTCATCGGAATGCGATGGC
AACACTGAACTACGAGCGCATCCTGCGCCAGCATGACTGTTTCGACTACGTGCTGCTGGCGACGGGGANGTAGCGTT
CACCAAGCTGGCCTTGGCCCTGGCGAATGACCTGCGGTTGACGACTCCCGGGACTAACCCGCCGTANTGAGCAAGGAC
AGATTCTGCGCACACCCTCCTCGTGGTGCACCTTGACA (SEQ ID NO. 653)

Clone Rv79

.....Rv79SP6.seq:.....
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGCCGGTGATCTGGGTGGC
CAACTCGGCGGGACCATCTCCATCACGACNGCAAACGCTCCGGCTTCGGCGACAGCGATCGCGTCTGCGATNGTTTG
TTGCGCGGCGTCTCCGCGGCCCTGCACCCGGAAGCCGCCCAAGGTGTTGACNCTTTGCGGGGTGAAGCCGATGTGTG
CATCACCGGGATNCCCGCGCGGTGAGACANGCGATTTGCTCGGCCACCCGCTCACCGCCCTGCANCTTGACNGCATG
TGCGCCCGCGTCTTGAAGAAACGGTGGCGNGGCAACCC (SEQ ID NO. 654)

.....Rv79T7.seq:.....
CGTTGAGATCCAGCTGCGCACTGTGCAGCGCCTCGGTGGTCTGCTCGGCCGCGGGATAACTCGTTGAGCTTGGCCA
GCGCGTCTGCGCCGATCAGCCAGCACATTGCGCGCCAGGACGCCGAGGAGACGGTGAAGCTCGCAAAGAAACCTA
TGGCGGACCGCATGATTACAGCGCGATCAACCACCTCTGGTCGAGCCTCAAAATTTGCTTCTTAAACGGGCCATCG
ACGGATGACGTGAGCTGGTTAGGTCTCAAACAGGTACGAAACGATCTCGGAATTGTCCAAAAGGGGAAGTTAAGA
AAATGGATAGATTTTACCATTTCGCTGTGGACGATCGTACTTCTGCTATAGGGCTCCAGGGGCATGCACACGCAACG
ACCTTACGCGACACCGGATCCGCGTGGCGCGGAACGGCACCCANGCGCAACCGAAGGGCCAATCCGACATCGG

(SEQ ID NO. 655)

Clone Rv7

.....Rv7SP6.seq:.....
ATACTCAAGCTTATCTAGGCGCCAGCTTGATTGGTCTGGTTGCATTGGCCAGCTGCGCGAGCCTGGCTCACTTCAACT
ACAACAACCGCAAACAATTGCCGCTTCGGATCCGAGTTCCGGTTGGGTACGCGGCAATGGANCAACATTTCTCGGTGA
ATCAGACTATTCTGAGTACTTGATCATCCACTCTGCACACGACCTGCGAACCCCGCGCGGCTTGGCGACCTGGAGC
AGCTGGCGCAACGTGTAGCCANATCCCAGGCGTTGCCATGGTTCGCGGTGTGACCCGGCCAAACGGGGAAACCTTG
AACAGGCCCCGGGCGACATACCAAGCCGGCCAAGTTGGCAACCGGCTGGGCGGCGCGTCCGGAATGATCGATGAGCGCA
CCGGCGACCTGAATCGGCTGGCATCGGGTGCCAACCTGTTGGCCGACAATCTCGGTGACTTCGCGGTCAAGTCAGCCG
GGCGTTGCGGGTGTCCGAGCCTTGTCAGCCCTCGCTTACTCCA (SEQ ID NO. 656)

.....Rv7T7.seq:.....
CAGGCATGCAAGCTTTTGGAGCGTCGCGCGGGGAGCTTCGCCGGCAATTCTACTAGCGAGAAGTCTGGCCCGATACG
GATCTGACCGAAGTCGCTGCGGTGCAGCCACCTCATTGGCGATGGCGCCGACGATGGCGCCTGGACCGATCTTGTG
CCGCTTGCCGACGGCGACGCGGTAGGTGGTCAAGTCCGGTCTACGCTTGGGCTTTGCGGACGGTCCCGACGCTGGTC
GCGGTTGCGCGCGAAAGCGGCGGGTGGGTGCCATCAGGAATGCCTCACCGCCGCGGCACTGCACGGCCAGTGCCCG
CGGCGATTGAGCCATCGGGACATCATGCTCGCTTACTACTCTCGACCAATCGCGGGAACAGCTCGATTCCCGGAACG
CCACGCATGGTG (SEQ ID NO. 657)

Clone Rv80

.....Rv80SP6.seq:.....
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGTAGAAAAAGATCGGTGA
GCGCATCGATTGCTCCGCCGGGTTTGCCGCTGCGCGGGCGAGCTGCCGTGACCGTCTATTTGGGTGATCAGATACT
GGGCTAGTTCCGTTGCGGGTGGGTGATCGAAGATCGCGGTGGCGGCGAGCGTTACTGCGGTGACAGCTGTTAAGCGGT
TACGTATCTCCACGGCACTCAAGGAATTAATCCCGAATCGGCAACGCCTGGCCAGCGTCNAGTCCGGCAGCGCCGT
CNCGCCCAGCACCGCTGCGGCATGCTCACATACCCTCGATCGCTGCGGCGANTTGCTCGTCNGCCGACCGACCGG
CCANCCGGGCGGCAAACCCNGAAGACCCAAGAATTCATCACCACCATCGCTAGC (SEQ ID NO. 658)

.....Rv80T7.seq:.....
CCTTCTTGACACCCACCTCGCCATCGACCTTGAGCACTCCGTGCTAGTTGGTGAACATGTGACCGGCGATCGGGCGGG
TGAACGCTACTGGGTGTGCGGTGTCGACGTTCTTACCACGCGGTAGCGCAGCGCCTCCTCGATCTCCGACTTAA
GCGAACCCGAGCCGCGGTGGAACACGAAATCNAACGGCTTGGCGTCNGCCGGCAGTCCGAGCTTGGCCGCGCCACCT
GTTGCCCTTGGCAAGGATGTCNGGGCGAANCTTGACGTTGCCGGGCTTGTANACGCCATGCACGTTGCCGAACGTCN
CGGCCAGCANGTATTTGCCGTGCTACCGGCGCCCANCGCCTCGATGGTTTTCTCGAAGTCTCCGGGCTGGTGACA
GCTTCTCGTTGATCTCGTTCGCCACGCGCTCCTCTCGCCGCGGACG (SEQ ID NO. 659)

Clone Rv81

.....Rv81SP6.seq:.....
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTGGAAAGGAGATCCCCGGG
AACCTGGTGGCAACCCCGCCATTGGGGTTGTTGGGATTGCCGATCAGCGTGAANGAAAGCTCGTCTGGAGACAGCGGG
TCGGCCGAAGCCGCAAGATTGGCCATCACTAGTGACGANATCGTGGCGCTCTGCGAGTANCCNAAGACAGTGACGTTG
TTNCCGGCGGCAATTTGCTGCCGAATCGCACTTTCGAGAATGACNGCACCTGCGCCACCGANGAATCNAAGTGAGG
TTCTTGATCAGACACCGGGTNGAGCCTTGGGGCGTGAAGANCGCCTGCGCNATAACACCCGGGACGCTGCCACTC
ATGTNCAGCGCGTTCGCGANCTCNACATATCT (SEQ ID NO. 660)

.....Rv81T7.seq:.....
TCCTGGTGATCGANGCGCGGTTCCGGCCGAAAATCCGGTTCGGGTTCCGGTTCGCGGTTCCAACCTTGANCGCGGTCC
GCAGCTGATTACCGTGGCAACGCCGGCCAACTGCGCATAATGCGCATCCGAACCTCACCCGCCCCGCCGATCA
CCCCAACCTGATCCAACGACAACCGCCCTCCCGCATACCCGGGCGCAGCGCGGAACTCCGGCAACCGCCGCGCA
CCGTGGCGATCGTGTGGGCGTTGCCGTGACGAACANCCATCTTCCAGGCCACCAACCCCGCAGACCGGCGCCCCG
TCACACCCCAACAACCGTCCGATCCAGCTCAGCCACGATCTCCACAATGCGCCCATCAATCGCATTGCGCTGAACGG
GCAACTCCGCCAACTCCTCAA (SEQ ID NO. 661)

Clone Rv82

.....Rv82SP6.seq:.....
AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGATCTGGTACCCATCCGTGATA
CATTGAGGCTGTTCCCTGGGGTTCGTACCTTCCACGAGCAAAACACGTAGCCCCTTCAGAGCCAGATCCTGAGCAAG
ATGAACAGAACTGAGGTTTGTAAACGCCACCTTATGGGCGAGCAACCCGATCACCGGTGGAAATACGTCTTCAGC
ACGTGCAATCGCGTACCAACACATCAGCATATGATTAATTTGTTCAATTGTATAACCAACACGTTGCTCAACCCG

TCCTCGAATTTCCATATCCGGGTGCGGTAGTCGCCCTGCTTTCTCGGCATCTCTGATAGCCTGAGAAGAAACCCCAAC
TAAATCCGCTGCTTACCTATTCTCCAGCGCCGGGTATTTTCTCGCTTCCGGGCTGTATCATTAACCTGTGCAA

(SEQ ID NO. 662)

Clone Rv83

.....Rv83SP6.seq.....

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATAGAATACTCAAGCTTANCGCCACCTCCCGGGCG
GAACTCCACGGCGTGGATNAAGGTACCGGCCGGGATGTTGCGCAATGGCAGGTTGTTGCCCGGCTTGANGTCCGCGTT
AGCGCCGGATTCCACCACATCCCCTTGCGAAANTCCGTTGGGTNCNATGATGTNNCGCTTCTCCCNCTCNANATAATG
GANCAACGCNATCCGTGCGGTACGGTTCGGGTCTACTCCATGTNCGCGACCTTGGCGTTGANACCATCTTTGTCAAT
GCGGCGAAAGTCNATCATCCGCTNAGCNCGNATGANCGCCGCCCTTGTGCCGGGTGGTAATCCGGCCATGCGCNTT
CGCTCCACCGCGAACGTGCAACGGGGGCNCCACGANTTCTCCNGGGTGAACCGGTNATCT

(SEQ ID NO. 663)

.....Rv83T7.seq.....

TGTGTGTTGGTGGTAACCATCTGAGCAGTGTGCCAAACCGGGGCAGCCAGCTCCCAATTGACGTGAGCCCGCTCACTT
GCTGGGTAAGCGTCG

(SEQ ID NO. 664)

Clone Rv84

.....Rv84SP6.seq.....

AACAGCTATGACCATGATTACGCCAAGCTATTTAGGTGACACTATANAATACTCAAGCTTGC GGGTNATNGCCTTGGT
CAACGGCACCGTGATCGGATCNGGGTCTACCGCACACATNGACTGGAGCTTCGGCGAANTCATCGCCTATGCCTCGCG
GGGGGTGACGCTGANCCCNCGGTGACNTGTTGNGCTCNGGCACGGTGCCACCTGCACGCTCNTNAACACCTCANGCC
ACCGGAATCATTCCNCGGTGGCTGCACGANAGCGANNTTGTNCNCTCCAAGTCTAAAGGCTGGGCGANANAAGCAN
AACGTCCCGACNAACGGCACTCCTTTTCNNTTGTCTCTC

(SEQ ID NO. 665)

.....Rv84T7.seq.....

GAAATCATTGATGGTTTGTAGTCACCAGGCCGATCAAGCCTTCGCCGAGCCAAATCCAATCAAGAGGCCAAGCCCGT
ACCAATCAGCCCGGCAACGAGGGATTCGCTCATTATCAGCCAAAATAACTGCTCTCGGGTTACACCCAAACAGCGCAA
TATGGCGGAAAAACGGTCGCCGTTGCACGACATTAAATGTCACGGTATTGTAGATTAAAAAGATACCCACCAACAANGC
AATCAAACCTGAGAGCGGTTAAATTGACCGTAAAGCGTCCGTCATCTGTTTGACNGTGTCCCGTTGGGTATCCGACGT
TTCCATACGCACACCGGCCGGCAGTCTTTGTTGGATGCGTNTTGCAATGGCCTCATCTTTGATGATCAAATCGATGTN
GCTCAGTCTTCGGGCATATGGAACAACTCTTGGGCCGTGGAAATATCAGCAATGATA

(SEQ ID NO. 666)

Clone Rv85

.....Rv85SP6.seq.....

CTTTTCGCCAGGCCGGCGCGGATGTCCTCATCGCTTCACGAACATCATCCGAGCTTGACGCTGTGCGCGAACAGATCC
GCGCTGCCGGCCGCCGCGCCACACCGTTGCCGCCGATCTGGCCCATCCCGAGGTGACCGCGCAGCTGGCTGGTCAGG
CCGTGCGAGCTTTCGGGAAGCTCGACATCGTCGTCAACAACGTTGGCGGCACCATGCCAACACGCTGCTAAGCACCT
CGACCAANGACCTCGCGGACGCCTTCGCCTTCAACGTGGGCACCGCCACGCGCTGACCGTGC GGCGGTGCCGTGTA
TGCTGGAACACTCCGGCGGCGGCAGCGTGATCAACATCAGCTCCACCATGGGCCGGCTGGCGGCGCGGGGTTTC

(SEQ ID NO. 667)

.....Rv85T7.seq.....

TGTGGGCTCCGATCCGGCGCGCATGGCATCGACGGCGACGCCGATCGATGACGGCCAGGCTTACGAGCTTGAGGGTGT
GAAGTTGTGGACCACCAACGGTGTGGTAGCGGACCTGCTAGTGGTTATGGCGCGGGTACCGCGCAGTGAAGGGCNC
AGGGGGAATCANCGCCCTTGTGCTCGAGGCTGATTGCGCCGGGATCACCGTGGAGCGGCGCAACAAGTTTATGGGACT
GCGTGGCATCGAAAACGGCGTGACCCGGCTTCNTCGCGTCAGGGTGCCCAAAGACAACCTTGATCGCANNGAAGCGACG
GTCTGAAGATCGCGTGACCACTCAACGCCGACGGCTGTCCCTACCGGCGATCCAACCGGAT

(SEQ ID NO. 668)

Clone Rv86

.....Rv86SP6.seq.....

GAGCTGGCCGAGCTGGACCGGTTACCGCGGAACCTACCGTTCTCGCTCGACGACTTTCAGCAGCGGGCTTGACGCGCG
CTGGAACCGCGCCACGGTGTGCTGGTGTGCGCGCCGACCGGCGCTGGCAAGACAGTGGTCCGCGAGTTCCGCGTGAC
CTGGCGCTGGCGGCCGGCAGTAAATGTTTCTACACCACGCCGCTGAAAGCCCTGAGCAACCAAAAGCACACCGATCTC
ACAGCACGCTACGGCCGTGACCAGATCTGGCTGACCGGTGACCTGTGTCGTCGACGGCAACCGCGGTGGTGGTGA
TGACCACCGAAATGCTGCGCAACATGCTCTAC

(SEQ ID NO. 669)

.....Rv86T7.seq:.....
GATCTCTGGATCGGCGGGGCTCTCCGGGCCGGCTCGGGGACCTCAGCGGGCCGCGCTTCCGGCCGAACCATTCCTT
AGCCATAGATGACCGCACCTCGATGCACGGTTTGGCGGCAACGCGGAAGGCGTCNGTCGGGCCCAGCCGCGGCAATG
CGGGTACCCGGGAGCGCGGGTCNGTANACCANCCTGGACTGCGTCGCGCGGTGCGTCNACNTCAAAGTCCCCGGCGT
CCCATATCGCGTATGACGCGGGCGCGCCCGGACCANGGTGCCGATCCGGCCGTCTCGAACACCACCGCCCCGCCAG
CCGCGCGGGTCCGGCAGCNAACCCGCCCGGCCGATACCCGCTGCCCGCGTGCCTGATTGACCGCCGCGCGCACGCT
GGCCANGGATCAAAGCCCGTG (SEQ ID NO. 670)

Clone Rv87

.....Rv87SP6.seq:.....
GGACCGGTAGCCCGCCAGGCGGTTCAGGGTGCCCTTCCAGTCCACGCCGCTGTGGTTCGGCGAACCGCTTATCTTCAAT
CGAGACGATCGCCAGCTTCATCGTGTGGCGATCTTGTCCGAGGGCACCTCGAACCGCGCTGCGAGTNCAGCCACGC
GATCGTGTGCCCTTCGCGTCGACCATCGTCGATACCGCAGGCACTTGGCCCTCGAGCAGCTGGGCCCAGCCGTTGGC
AACGACCTCAGANGCAGGATTGGACATCAGCCCTAGCCCGCTGCGAACGGGAACGTCAGCGCAGTGGCGACGACACT
GGCCAACAGACAGCACCCAGCCAGCTTCAGAACGGTGATCGCGGCCGGGAAGCGCTCGGGCATGCGTNCCTACAGTAGC
GACCTCCTGTCACTCCACGTGCCGCTCGGTCCAATAGAATCTTCCGCGGGCGGGTGAATCTCTGCNGGATCGGGGCN
GGCGC (SEQ ID NO. 671)

.....Rv87T7.seq:.....
GCTCGTTGCCGGCGCGATCTCGTCGAGCTCGTCTTCCATCGCCGCGGTGAAGTCGTAGTCGACGAGCCGACCGAAAT
GCTGCTCGAGCAGACCGGTTACCGCGAACGCCACCCATGACGGCACCACTGCACTGCCCTTCTTGTGCAGTNGCCGC
GATCTGGATGGTCTTGATGATCGACGANTAGGTGACGGGCGGCCGATGCCAGCTCCTCGAGCGCTTTGACCAGCG
ACGCTCNGTGTNNCGGGCCGCGGGTTGGTGGCATGGCCGTCTGGGGTCAACTCGACNATGTCCAACCGTTGACCCG
GGGTGAGATGGGGCAGTCGCCGCTCGGCATCGTCAGCCTCGCCGC (SEQ ID NO. 672)

Clone Rv88

.....Rv88SP6.seq:.....
GTCTTTTCGATGGCTGCTTCTTCGGCGCTGACGCTGGCGATCTATCACCCCCAGCAGTTTCGTCTACGCGGGAGCGATGT
CGGGCCTGTTGGACCCCTCCAGGCGATGGGTCCCACCTGATCGGCCCTGGCGATGGGTGACGTGGCGGCTACAAGG
CTCCGACATGTGGGGCCCGAAGGAGGACCCGGCGTGGCAGCGCAACGACCCGCTGTTGAACGTNGGAANCTGATCG
CCAACNACACCCNCGTCTGGGTGTACTGCGGCAACNGCAAGCCGTGCGATCTGGGTGGCAACAACCTGCCGGCCAAGT
TCCTCGAGGGCTTCGTGCGGACCATCAACATCAAGTTCCAAGACGCCTACAACGCCNGTGGCGGCCACAACCGCGTGT
TCGACTTCCCGG (SEQ ID NO. 673)

.....Rv88T7.seq:.....
GCCAGGTTCGAGGTCCCATGCGCGTGGGCCATTGATGCTGATCGCCAGGACGTCAAANATTTGGTCCGGCGTCAGCTGG
GCGAAAAACGTGGGCCCCAGGACTTGGCCGGAGCTGCCGGGTTCCCGTCGCGCAGCTCGGCGGCCCGGTGAGAAAN
AAATTGCGCCAGGTTCGCACACTCCGCGCCGTANGCCAGCTGCTCCAGGGTGTTCGGCATAGAGCCCGCGGGCCGACGG
TGCTCGCTGTTCGGCAACACCGCATGGTCGAGAAGCGTTGCCGCCCAACGGAAATCACCTGCGTCNAANGCTTCGGCG
GCCAACTCCAGCACTCGGTTCGATG (SEQ ID NO. 674)

Clone Rv89

.....Rv89SP6.seq:.....
NAAACGTTCCGGCTTNGGTGCCGGGCGCTTATTGCGTCTCTGGGATCACNCTCAGTCGCCGGCGGCTGCCGTTGGGC
TATNANTTGCACCGANCCGGAATAATCCGCACNANAAGTGCNAGTAGCGGCCTGCAGAANTGCATCCTCGGCGAANNG
ACTACCGGTGGACANCNACAAGCGCCGCCGAACAACGCACTGGCCCCAGGGATNGGCGTCTATCGGCCCCGCGCGTCCG
AACTNGGAACAGACNGTGGGTTTACCGTGATCTGGTGGGAATGCTCNACCANACCTCCCNANNGCTACGGAACNA
CGGCGGATATTNCGCNTCCCANCTCGAGCCTGACNCTNGATATCGTCGANNCTCACCATCNCGATCNGCTGTGCCG
GTNTTGCTCGGACTN (SEQ ID NO. 675)

.....Rv89T7.seq:.....
CGAACGACGAACNCCNCAAGCCATGGTGGTTGGCGCCGTCAAAAGGTCCGCGGTGCGCCACTACTGGAAAATCGCCTTG
AGCGTCNCTCGACNCCGCTCGAGTTGGGTGNTAACGAAATACCTGATGCCGATCANGTCNACGTCTCCGTGCGNCC
AACGTGCAGCGGCGACCACTCTACNANGTCTCGGTNCCGCCNCGGCCAGNGCACCACAGTGACNAATCCNTGCCGC
NTCGGGCCNAGCANTCCCGGTGCNACCGNGGTGGTCCGGCGATGGTNGGGTGTNCTCNNTACNGGAACGCCAGCGCN
ATCANCATCGGCANACTCNCGTCGATGTGCCGCGGCGCAACCATCCCCACAATGATCNGGTGCGTCTGATCAGGCN
(SEQ ID NO. 676)

Clone Rv8

.....Rv8SP6D.seq.....
TTAGGCGTGACGGCCACCGGGGCCACTCCGCACAATCTGTACCCGACCAAGATCTACACCATCGAATACGACGGCGTC
GCCGACTTTCCGCGGTACCCGCTCAACTTTGTGTGACCCCTCAACGCCATTGCCGGC (SEQ ID NO. 677)

.....Rv8T7D4.seq.....
CGTCACCCCGATGCGCCAGATCGGGGCTTCGCAGATAAAGCACGAACTGGCGGGCAAAACGTCGATCTCGGAGCCGG
AAGGGCAATCAGCCGACCGTCGACGAACGACACCGGCGAGACCACTTAGGCAGTGACGGCCT (SEQ ID NO. 678)

Clone Rv90

.....Rv90SP6.seq.....
CTTTTCNCGATGTCTCATGATNCCNANGGAGAACNNTGCNANCNCNGCCGCTGACNTNGCNCACCGCTNTGGCNGNGG
TGACATTGGTGGTGGTTGCGGGCTGCNACGCCCCGACTCGANGCCGANCCATNTNTTGGCGCCGACCGCNTNTCGTCTC
NACCGCANNNCCNATCTCNGCCGCNCCCGGTGGANCTACNGCTNCTTCGCCATCTCTCGCCNATGGCTCCNGCGNNTC
GCNCAACGNTTGGTTTGGTNANCTGCCTACCTGGTCT (SEQ ID NO. 679)

.....Rv90T7.seq.....
GCTGCGCCAGTCGTTCGGTGCGGTGATGCCGTTGGACCNACCATCGGAGTTAGTTGCCGAACCGCGGACCACCGCAAG
CACCCGGTCTTGGTTCGCGCACCGCGTTCGGCCAACCGCTTGAGCACCACACGCCGCGAGCCCTCGCCGCGCACGAATCC
ATCCGCGTTGGCGTCNAANCTGTNGCATCGGTGCGTTCGGTGACAGCGCCGACCACTTGACAGCGCGATGGCGGTGAA
CGGTNANTAGGTGACCTGCNCCNCGCCGCCAATGCCACCTCCGCTTCACNCATGCGAATGGTCTGACACGCCNAG
TGAATTGCCACCAGCACAACAAAATCGGTATCTNCGCGCAGCGCGGACACGCNATCCCNACTGATACTCGATCCGC
CCCACCGCTTGNANCTCCGGGTTCCNGTGCTCATGTACNCTCATGTGCGTCTGCGCNCGATATTGACGATCGTGTTC
CCACGANNANAGANCCTCATCACGCCGGTTCGAGTGCCG (SEQ ID NO. 680)

Clone Rv91

.....Rv91SP6.seq.....
CTGTGTGCGGNCGGCGCGATATCGGCCCTTTTACTAACCGAACCCGATGTGGGCTCCGATCCGGCGCGCATGGCATCT
ACNGCGACGCCGATCGATGACGGCCAGGCTTACGAGCTTGAGGGTGTGAANTTGTGGACCNCAACGGTGTGGTAGCG
GACCTGCTANTGGTTATGGCGCGGGTACCGCGCAGTGAANGGCACCGAGGGGAATCANCGCCTTTGTCTGTCTANGCT
GATTCTCCCGGGATCACNTGGAGCGCNCNCNANTTTCATGGGACTGCGTGGCATCCAANACGGCGTGACCGGCTTCA
TCCNTCNGGGTGCCCAAAGACAACCTTGATCNGCNGGAAGCGACGCTGAANATCGCGCTGATCNCACCTCAACGCCGG
ACGCTGTCTACCGCGATCGCACCGGANTTGCCANCCGCGCTNANNATNCGCGNGAATGNCCGTCCACNANTGCAT
GG (SEQ ID NO. 681)

.....Rv91T7.seq.....
TGGGGTGCCGGGCGCCGAGTTGCGTCCCTGGGATCACGCAGAGTCGCCGGCGGCTGCCGTTGGGCTATGAATTGCACC
GAGCCGGAAAATCCGCANCAAACTGCGAGTAGCGGCCCTGCAGAACTGCANCTCGGCGAAACGGAGTACGGTGGACA
ACGAAAAGCGCCGCCAACNACGCACTGGCCCGAGGGATTGGCGTCAATCGGCCCCGCCGTCGAACTTGAAGANAC
ANTGCGGTTCTACCGTGATCTGGTGGGAATGCTCCAACNNACCTTCNCCGAAAGCTACGGAAGCNACGGCGCGATNT
CGGCCTTCCAGCTCGACCTGACGCTGGAAATCG (SEQ ID NO. 682)

Clone Rv92

.....Rv92SP6.seq.....
NGGCNNGGAAGTTAATGCCCTACTGGTTCNATGCTCNCACNTCNCNGTGACNNCCTGCNCCGACCCGCGGAGGTCCT
GNCCGTNACCACCGANCGGCGATCCGGGACTCTNGTACGCATCCAACANNGANCAACGTGCACGGGCGGAGTNGTNC
CGCCACTTCGNCNATGACGGGGTTCGATCCNTTCGACGTCGCTCGCCGCGTGGTTCGAGTGGCGGTACNCTCCNNGTA
CTCGACNCACNAGCAGAGGACTCGANCCATCTACGTGTGGACGAAACANATCTTCTGTCNACGACTACACCACC
ACCCAGGCCATCGCCGNCGCCGCGANGCCCTTCGACGCNCTACTGGTCCNNGNGGCGCTCTCCGGTTGTCTNNC
NCNTGNCGTGTTCTTACNCACTGCCNACATCGANCCCGAGCNATNCNANGTCCGTCAATC (SEQ ID NO. 683)

.....Rv92T7.seq.....
GGACACTGTTGCGGTGCCCCCTCGTCAAAGCCGGAGTGGTCTGTGCGCCGGACCCGACCCGACCTTCAGCGGGGGTT
CACAGCTCCGTGGGTGCCGTTACTTCCGATCGCCGAGTGTGCGCGTGCCTGTGGCTGATGCTGAACCTCACCGCGTT
GACTTGGATCCGGTTCGGGATCTGGCTGGTGGCGGAACCGCGATTTATGTCNGCTACGGGCGCCGCACTCGGCGCA
TGGCCTTCGGCAAGCNANANAACGCGACCCGGAGGTGTTGAACTAGCTTCGCCGCGTATTTACAAATTGCNTTATA
TGTCTACACATAAGACGCAAACCTGCTCTATTGTCAANTCCANCGTGGTGTGGCNATGAAGATGTTTGG

(SEQ ID NO. 684)

Clone Rv94

:Rv94SP6.seq:::

TCCTTCTCGGTATCGGTTTGGGCTGTCACCANCAGTTGGTAGTTCTTCACGTNCTGTTGTTTCGAGCGTCNAGCCGTCG
CGCGTGTGNANGTCNCCGGACGCGTATCCCGCCAGGCCGGTCANGGTGCCCTTCCANTCCACGCCGCTGTGGTCGGCG
AACGCTNATCTTCAATCGAGACCATCGCCAGCTTCATCNTGTTGGCGATCTTGTGTCNNACGGCACCTCNAACGGCGCT
NCTAGTACNCCACNCNATCNTGTTNCCTTCNCGTCNACATCCTCGATNCCNCNTGCATTTCCCTCGANNCCTGGGC
CGAGCCGTTGGCANTNACCTCNGAGCCCCATTGGACATCANCCANCCCGCCTGCGAACGGGAACGTGAGCNCNCTGG
CGACAACCTGGCCAACAN (SEQ ID NO. 685)

:Rv94T7.seq:::

CACNCCGTGATCGCNAGCCCCNGTAGAAATNGTTGAGCCAGTTGGTGCGGCGCTCGTTGCCGGCGGTNATCTCGTCGA
GCTCNTCTTCCATCGCCGCGGTGAAGTCGTACTCGACNAGCCGACCNAATGCTGCTCNAGCAGACCGGTTACCNNA
ACNCCNCCTCNGTACNGCACCAGTGCNCTGCCCTTCTTGTGCACGTACCCGCNATCCTGGATGGTCTTGATGATCNAC
TANTNTGTGACGGGCGGCGGATGCCATCTCCTCNAGCGCTTTGACCAGCGACNCCTCGGTGTATCGGGCGGCGGG
TTNGTGGCATGGCGCTCGGGGTCACTCNACNATNTTCANCCGTTGACCCGGGGTCACA

(SEQ ID NO. 686)

Clone Rv95

:Rv95SP6.seq:::

TGGCCTTCTTGNANGGCGNNACATNNGCTATNGCGAGCGTGTAACCGATCATCNTCCNNGGCGACTGTGGCCTGANG
GCAAGGGTNGCCTNATTCNTCCTCCTGNGGCATGGTTNCCACACGGAATGNCGGTAAGTCTGGTCGGCAACCTGGCCC
GCTGCGGGTTGGGTTTCGGATTTCGCTCGGCTANTAAAGGTGCTCGCCTGGTGTCNACTAATCNCNATATACNCTTANC
GGGAGTNGNCGTCCCGATCCTNGCCCTGCCGCGGGGATCNCGTTTCGCANACCCGCCACCGGAACCTCNCAANGTGGC
TCATCGGGCTCTACGCGCATCTTCCCGGATTCTTCGCGCGCNGNTNCCGNGGGACCCCGGACTGTGACNGGCCCA
CGGCTCATCATCG (SEQ ID NO. 687)

:Rv95T7.seq:::

CCGGATAGCGGTGTCTGAACCTTCGCCCCGTTCCCTCCANCGCATTGAGCTTCAGCCCGACCGGCAGGTNNGGAGTCGGC
ATGCGGTCTTTCGCCCCGACCCCGCTGGCTAAATANCCACCCCGAGCGCGGTACGGTCTTTGCACCGGGACGACGC
ATACCGGCAGCGCGAACATCNCGCGGGGCTGCAGCNTGAACGTCCAATACCANTCNAACAGTGTCCGCGCGTNAAC
CCGANCCGGCGGTTCGTTTNGTAATCAACGGCTCCTGCGCAACAGCTGCAAGTTCGCGGTGCCACCGCGGTTGACGA
TCTTGATGTCTGCGANCTCGCGCACCAGCTCGACGGCCCGGCA (SEQ ID NO. 688)

Clone Rv96

:Rv96SP6.seq:::

CCTCCCGACCATACAGGCAAAGTAATGGCATTACCGCGAGCCATTACTCCTACGCGCGCAATTAACGAATCCACCA
TCGGGGCAGCTGGTGTGATAACGAAGTATCTTCAACCGGTTGAGTATTGAGCGTATGTTTTGGAATAACAGGCGCAC
GCTTCATTATCATCTCCAGCGTGGTTTAATCAGACGATCGAAAATTTTCATTGACAGAGGTTCCCAAATAGAAAG
AGCATTTCTCCAGGCACCAAGTTGAAGAGCGTTGATCAATGGCCTGTTCAAAAACAGTTCTCATCCGGATCTGACCTTT
ACCAACTTCATCCGTTTCACGTACAACATTTTTTAGAACCATGCTTCCCGAGGCATCCCGAATTTGCTCCTCCATCCA
CGGGGACTGAGAGCCATTACTATTGCTGTATTTGGTAAGCAAAATACGT (SEQ ID NO. 689)

Clone Rv9

:Rv9SP6.seq:::

CTTCACNTCCGTACGGCTCGGGTACGCTTCGGTCNCATTGTGCGAGTGATAGATGACGACCGGGACCTCGTCGGCATC
TTCCATAGCCCGCCACACCTTCAGTTGCTCACCGGAATCCAACCGGTANAAGGTCGGCGANCGCTCNGCATTGGTCAT
CGGGATATGCCGCTCGGGACGGTCANAGCCCTCGGGTCGGGCGAGCACTCCGCAAGCTTCGTGCGGGTGGTCGCGACG
CGCATGGGCCACCATCGCATTACCAAGGTCTGCGCGAATCACCAGCACGTANACGGTTTCCTTTCTAAGCAACACCGA
ANTTTTCAGGACCCGAATGCTCCGGGAAACATGTCACGGTAGGTGCGGTATTCCGGCTACCGGCTGANCATTGAGCACGC
CGGCCAGCACCGCACGAACAGGCAATCAGCCGCCGCCGACCCGACCGCGG (SEQ ID NO. 690)

:Rv9T7.seq:::

CAGGCATGCAAGCTTGATGCCGCCGAAACCGAGCGTGAGCACGCCGCCAGCCACCACGCGCGGGTCGGGCGCCGGGCC
CGGGCCGCCAGGCTGCTCCGCTCGGTGATGGCACGCCACCGCGACACCACCGGCTGCGCTACGTGAGCCATACCGG
GCGGAGCTACATCGGCTCGGCCGCCAGTGTTTCGGGCCCTCTTTTCGAGGTGAGGTCGATACCGATTTGCGCATCCGC
AGCCGCACCTGGACGACAGAACCCTGACGAATTGCTTGTGCGGGCGGGCCAAAGAACAGCTTGGCATCCTGGC
GCGATTGGCCGCGCGGCGCTGGTCGCAAGGAAGACCGGTTCCGGTGCTGAT

(SEQ ID NO. 691)

Table 4 : End-sequences of the polynucleotide inserts cloned in the named recombinant BAC vectors contained in the I-[XXXX]²⁰⁴⁹*M. bovis* strain Pasteur genomic DNA library.

RvXXXSP6 corresponds to the SP6 end-sequence of the clone RvXXX.

RvXXXT7 corresponds to the T7 end-sequence of the clone RvXXX.

RvXXXIS 1081 corresponds to a region located close to a copy of the IS1081 repetitive sequence (Insertion element).

The character « - » denotes an uncertain base residue.

Clone X0001

.....X0001SP6.seq:.....

AAG-

TCGGGTTTCCACACGCGCGGTTTGACCCTAGTCATATGTAATCATGTGTACCATGTGCGGGCGCTTTTCGACGGCCG
CGAACCACCGGA-ATTTCTGTGATTTCACTGCATGCGTACCATCTGGCACAATTGAGCA-TTGTCT-
TCGCGGTGGTCGG-CGGGTTGCGTGCCGCTGCTGCCA-ATGCACCA-
TAAGCCCGAACCCACGGCTTGGTGACCACCGCAGCTGCGTGTGGGGGTAACCACTCCGCGACCCCAAGGATGGT
CATTTCCAATGAACCGGCTGGACTTCGTCCA-A (SEQ ID NO. 692)

.....X0001T7.seq:.....

GTGCGGTTTCGATCGACCCGATCTTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTTTGGCTCT
ACCCACTCTTTGAGTGGCGCCGTCGCTGTGCCCCATCGGTGTTTCATGACGAACGCTTCGAAAGACTTCCTCTTG
AGCCGGAATGTCTGCGTAAAGAAGTTCCATGTCCGGGAAGTAGACCCGGTCGCCCTCCACGTGGTACTCCTTCGAGG
TCCGCTTCTCGCGGATCCGATAAACACCGGCCCCAGGCACCGCAGCGTGAGTTCGAACGGCTTCAGGTAGGTGTT
ATGCGGCGGACTCCGGGAGTGCAGAAATAGCGGTGCGCGTAGCTGTAGACCGGATGGTTTCCGCCCAGGCTGACG
TCGAAGATGCCTCCTTGAAGGGGCGCGA (SEQ ID NO. 693)

Clone X0002

.....X0002SP6.seq:.....

AACTCAAGTTTTACGGTGATCGCGCATCACCTGGTTCATGAACTGGAAGCAGCGCAGCGCTTCCTTTTCGGCCGCA
ACATGAGCCAGCCTCTCGTCGGCGGTGCGGTGCAGGTGCTCGGGCAGCTCGGCCGCGACAGCCGCTGACCTGAAA
CCAGCTTCCATATCCCAGCAG-
AACGACGCCAGTCCGCTACGTAACCCCTCCGCGACTGTCCATGGACAACAGCGGTTCTCCACCGACCGGGCCCGG
TGT (SEQ ID NO. 694)

.....X0002T7.seq:.....

GTGCAAGTTTCGACAATGTGGTGCCGGTTCGGCGGCTACGTGCCATCGAGACACTGGCGCA-GCTATCGCACCCGTT
ATCGGCTGCGAGCAAATCGCGGTATGCGTCTTGAGCATGAGTCGGCGACCGTCGTCATGGTCGACACCCACGACGG
AAAGACGCAGATCGCCGTCAAGCATGTGTCCGCGGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTC
GCGATGCCTGGCGCCCGCGCGGTGGTCGTGGTTCGGCTCGGATAGCGAGGTGAGCGAATTCTCGTGGCAGCTCGAA
AGGGTCTGCGCGGTGCCGGT (SEQ ID NO. 695)

Clone X0003

.....X0003SP6.seq:.....

TTCGAGTCATGCGCCCGCTCGACCACGAA-ATGCACGTCG-
GGTTTCGATCGACCCGATCTTCACCTCGTAACCTCGATGCTTAGCAGGATCCAGCTTGACCGCGTTTGGCTCTACCCA
CTCTTTGAGTGGCGCCGTCGCTGTGCCCCATCGGTGTTTCATGACGAACGCTTCGAAAGACTTCCTCTTGAGCCG
GAATGCTGCGTAAAGAAGTTCCATGTCGGGAAGTAGACCCGGTCGCCCTCCACGTGGTACTCCTTCGAGGTCCGG
TTCTC (SEQ ID NO. 696)

.....X0003T7.seq:.....
 GTCATGTGTACCATTTGCGGGCGCTTTTCGACGCGCGGAAACACCGGAGATTTCTGTGATTTCACTGCATGCGTA
 CCGTCTGGCACAATTGAGCAGTTGTCTGTGCGGGTGGTTCGGCCGGGTTCGCTGCCGCCTGCTGCGAGATGCACCAAT
 AAGCCCGAACCACCGGCTTGGTGACCACCGCACGCTGCGTGTGGGGGGTAACCACGCCGCGACCCCAAGGATGGTC
 ATTTCCAATGAACCGGCTGGACTTC-TCAACAA (SEQ ID NO. 697)

Clone X0004

.....X0004T7.seq:.....
 AACAGCGCGGTTGAACTGATAGGTGCGGCCCGGCTCGAGCAGGCGGGCCATTTGTTTCGATGCGGTTACCGAAAGAT
 CTCTTCGGTGACCTGCCCGCCGCGCCAGCTCGGCCAGTGCCTGGCGTTGGCCGCCGCGGCGACGATCTTGGCGT
 CCACGGTGGTTCGGG (SEQ ID NO. 698)

Clone X0006

.....X0006T7.seq:.....
 GCATCTGGGCTGGCGGTGGTTCGCGCTCCGAAGCCGTCGAACACCATCGCCAGCGGGCTTCCACATCAACGACCA
 TTTCGGCCAGCTTGGCGCGCATCAGCGGCTTGTGATGAGCGCCCCACCGAATGCCCGCCGCTGCCCGGCGTA-
 CACAGCGATTTCGACCAGCGCGCGCGCGCTTCCGAGGGCGAAGCGGTGCCCAACCGCAATCTGTTGGTCAG
 CTCCATCATGCGGTGAGTCCCTTGCCG (SEQ ID NO. 699)

Clone X0007

.....X0007SP6.seq:.....
 ATCGGTTTCCAGCAACAGCCGATCGACGGCTTCGCCCA-
 GGCGGCTCCCGGGCGACCCGACCATTTGCTGTGCGCGCTAACGCCATCACGGATGACGCGCAGTTCGTCGCTGTCTA
 GCTCCACCATCGCCTGCACACCGGCGGCCAG-ACCCATTGGCCGTGCGACTCGTA-
 AGCAGGTAATCCTCGTCGACGGAATCGGTAACACCGCGCCGCTCCGCTGCCAGGTTCGGCGGGGTGACACCGGC
 GGGCATCGGGATGGACGACGCGGCTGCTGACGGCGCCTGTC (SEQ ID NO. 700)

.....X0007T7.seq:.....
 AGCGGTTTCCCA-
 GCGGATGTGCTGTGAGCGCCGACCAACAGCGCCGACGCTAAGGATGGAACGCACGGCATCTTCTGACGCGTAACC
 GCGTTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTCTCGGAGGCCATCTGGGATGTTGATGTCTGTGAT
 CTTGAGCCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAAGCCGCTACCACCGTGACCTTCTCTGAGGA
 AACGCTGCGTTGGCTCTACGAGATGATGGTGGTCACCCGCGAGCTGGATACCGAATTCGTCAATCTGCACG
 (SEQ ID NO. 701)

Clone X0008

.....X0008SP6.seq:.....
 CAAGCTTCCACAGGTAGGGATCGAGGAACAGCGGTTGAACTGATAGGTGCGGCCCGGCTCGAGCAGGCGGCCATT
 TGTTTCGATGCGGTTACCGAAAATCTCTTCGGTGACCTGCCCGCCGCGGCCAGCTCGGCCAGTGCCCGGCGTTGGC
 CGCCGCGGCAACGATCTTGGCGTCCACGGTGGTTCGGGTTCATGCCCGCGAGCAGGATCGGCAGCGCGCGGTGAGCC
 GGGTGAACCTTCGTGAAAGCTTGACCTGCGCTCGGGGAGGCGAACCACGGTCGGTGCGTANCTCCACCAAGCCCGG
 GCAACCTCGGGGGTGGCGCC (SEQ ID NO. 702)

.....X0008T7.seq:.....
 TGGACCTCATGACAACGCGGCGGCGATTACCCCGCTACCGCCAGCAGCATGACGGCGGTAGCGAACACCGCCGGAT
 GCAGCGCAGGTGCGTCGATGTGCTCACGGAATCGCCCCGGCACCAGGATCTCGAGGATCACCAAGTCCACCCCTGCG
 AGCGCGACCGAGATTCCGTACACCGCCACCGGATCAGGCCCTGGGCCAGCTGGCGTATATGGCGGCGATGGTG
 ACGATGGCCAGCGCCACATACATTGTGGCGGCCAGAACCACGGCGTTGGGGCGGCGGTGATGAACACTAGGCGACG
 CAGATCGCCCGGGTCAACAGGTTGACCATCAGAAAGCCTGCGA (SEQ ID NO. 703)

Clone X0009

.....X0009SP6.seq:.....
 TTTGGTGGCGCGGCAATCAACTTC-GCTC-
 CAGCGGTTTCCAGGCGGGATGTGCTGTGAGCGCCGACCAACAGCGCCGACGCTAAGGATGGAACGCACGGCATCT
 TCTGACGCGTAACCGGTTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTCTCGGAGGCCATCTGGGATGT
 TGATGTCTGTGATCTTGAAGCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAACGCCGCTACCACCGT
 GACCTTCTGAGGAAACGCTGCGTTGGCTCTACGATATGATGGTGGTCACCCG (SEQ ID NO. 704)

.....X0009T7.seq:.....
CGCCCAGGGCCGCTCCCGGGCGACCCGACCATTTGCTGTGCGCCGCTAACGCCATCACGGATGACGCGCAGTTTCGTCCG
CTGTCTAGCTCCACCATCGCCTGCACACCGGCGGCCAGGACCCATTGGCCGTGCGACTCGTAGAGCAGGTAATCCTC
GTCGACGGACTCGGTAACCACCGCCGCCAGCTCCGCTGCCAGGTCGGCGGGGTTGACACCGGCGGGCATCGGGATGG
ACGACGACGCGGTGCTGACGGCGCCTGTCGCGACGCTGAGCTCGGACACAGCTAGTAAATGTAGCCTAACCTACTTA
ATGGGTCGACGCCCCCGGGTTCGTCGATGTCCAACGTTGCTCGACTGGAAGAAAATGCTCGTCGGGGAGCAAATG
GCACC (SEQ ID NO. 705)

Clone X0010

.....X0010SP6.seq:.....
AATACTCAATCTTGATCGGTTTCCAGCAACAGCCGATCGACGGCTTCGCCCAGGGCCGCTCCCGGGCGACCCGACCA
TTGCTGTGCGCCGCTAACGCCATCACGGATGACGCGCAGTTCTGCTGTCTAGCTCCACCATCGCCTGCACACCGG
CGGCCAGGACCCATTGGCCGTGCGACTCGTAGAGCAGGTAATCCTCGTCGACGGACTCGGTAACCACCGCCGCCAGC
TCCGCTGCCAGGTCGGCGGGGTTGACACCGGCGGGCATCGGGATGGACGACGACGCGGTGCTGACGGCGCCTGTGCG
GACTCTGAGCTCGG (SEQ ID NO. 706)

.....X0010T7.seq:.....
GGATGTGCTGTGAGCGCCGCACCACCAGCGCCGACGCTAAGGATGGAACGCACGGCATCTTCTGACGCGTAACCGCG
TTGTGATCGCGAGCTGAGGAGACGGTATGGGGGAGGGTTCTCGAGGCCATCTGGGATGTTGATGTCTGTGATCTT
GAGCCGGTGCAACTCGTCGGCCCGGACGGTACGCCGACGGCCGAACGCCGCTACCACCGTGACCTTCCTGAGGAAAC
GCTGCGTTGGCTCTACGAGATGATGGTGGTCACCCGCGAGCTGGATACCGAATTCGTCAATCTGCAGCGCCAGGGGG
AAGCTGGCGTTGTACACGCCCTGTGCGGGGAGGAAGCCGCGCAGGTGGGTGCGGCGGCTTGCTACGCAAAACCGA
CTGGTTGTTCCT (SEQ ID NO. 707)

Clone X0012

.....X0012SP6.seq:.....
ATCACGACAACAGCGACGGTGTGTCGGATCAGCGGCCCCCGTTGCCGGGCAATGTTGAGGCGTTTCTGCGTCTGGTT
GAGGCCGGCTGGGAC-
CCGAGGTGGCTCGTCGGCCACATGGGCAGCACACCACCGTGGTGATGCATCTAGACGTGCAGGACCGTGCCGCTGGC
CTGCA (SEQ ID NO. 708)

.....X0012T7.seq:.....
GCGGCTACGTGCCATCGAGACACTGGCGCAGGCTATCGCACCCGTTATCGGCTGCGAGCAAATCGCGGTATGCGTTC
TTGAGCATGAGTCGGCGACCGTCGTGATGGTCGACACCCACGACGGAAAGACGCAGATCGCCGTCAAGCATGTGTGC
CGCGATTATCAGGACTGACCTCCTGGCTGACCGGCATGTTTGGTCGCGATGCCTG:
(SEQ ID NO. 709)

Clone X00013

.....X0013T7.seq:.....
TACAAGCGGCACCTCGCCGGTGAACCTGACCGTTGCGACGCTGCGCACCCGCCCGGGCGCGTGCTCGGCGCGCCGGC
GGCCCCGAGGCCTGAGAGGGGAACCAACCATGCAGGTGAACATGACGGTAAACGGCGAGCCCGTCACCGCCGAGGT
CGAACCCCGGATGCTGCTGGTCCATTTTCTCCGTGATCAGTGC GGCTCACC GGAACTCACTGGGGCTGTGATACCA
GCAACTGCGGGACATGCGTGGTGGAGGTGACGCGCGTGCCGGTGAAATCCTGCACGATGCTCGCCGTGATGGCTCC
GGGC (SEQ ID NO. 710)

Clone X0014

.....X0014T7.seq:.....
AGCGGCTGGTTACGACTCCCTGTTGTGATGGACCATTCTACCAACTGCCCATGTTGGGGACGCCCCG-CC-
TCCGATGCTGGAAGCCTACACTGCCCTTGGTGCGCTGGCC-C-GCGACCGAGCGGCTGCAACTGGGCGC-
TTGGTGACC-GCAATACCTACCGCACCCC-ACCCTGCTGG-CAAA-
ATCATCACACGCTCGACTTGGTTAGCGCCGGTCTGA-CGATCCTCGGCATTGGAACCGGTTGGTTT-
(SEQ ID NO. 711)

Clone X0015

.....X0015SP6.seq:.....
ACGCGCGCCGATCATATCTGCTATGGATGTACAATTACGCTCTTGCTGTTATACCAGTATATGGTGTACTATTTGAT
CTATGCTGACGTGTGAGATGCGGGAATCGGCCCTGGCTCGACTCGGCCGGGCTCTGGCTGATCCGACGCGGTGCCGG
ATTCTGGTGGCGTTGCTGGATGGCGTTTGTATCCCGCCAGCTAGCTGCGCACCTCGGGTTGACCCGATCGAATGT
GTCCAACCATCTGCTGTTTTCGGGGCTGCGGGCTGGTA-TCCCAACCTATGAGGGCCGGCAGGTTCCGGTAT
(SEQ ID NO. 712)

.....X0015T7.seq:.....
 CCGCGCTGCTGCTGACGTCGGTCGAACGTGCGACACGTCTGCGAATACCGGCCGAACGCTGGGTTTATCCACAGGCT
 GGCACCGACGCCCACGACACACCGGCCGTGCGCGACCGCCACCGACTGCATCGGTCGACGGCCATTTCGGATCGCCGG
 TGCCCGGGCGCTGGAACGTGGCTGGGCTGGGGCTCGATGACATCGAATACGTGACCTGTATTTCGTGCTTTCCCTCCG
 CTGTCCAAGTCGCCGCAATCGAACTCGGCCTGGACACCGACGATCCTGCCCGCCGCTGACCGTCACCGGGGGCCTG
 ACCTTCGCCGGCGGGCCGTGGAGCAATTACGTACGCACTCCAT

(SEQ ID NO. 713)

Clone X0016

.....X0016SP6.seq:.....
 CAGGCGTGCAATGACCTGCACTGCGCGGA-A-
 TCCCTAACCCACTAAACCGGGGCGCTCACAAGCCGTGCAGCTCGGTGAGGTGCGCGACCGAGAA-
 TAAATGAGCAGACCCGTGCCGTCAACGATGGTGGCGATCATCGGCCCGAAACGATGGCCGGGTC-
 ATGCGCAACTTCTTCAGCAGCGCGGAAGGACGGCA-CCACCAGCGAC-ACCACACCACGAT

(SEQ ID NO. 714)

.....X0016T7.seq:.....

GCGAA-
 CACTTCGTCAACTTCCAGGGCTGCCCCGACCAAGTATTTTCGACGAGTATTTCCGTGCGGCCGCGCCGCGCGCGCGC
 GGCAGGTGGTCATCCTGGCGGCGGGGCTGGACTCGCGCGGTACCGGCTGCCTTGGCCCGACGGGACCACGGTTTTT
 GAGCTGGACCGCCCGAGGTCCTTGATTTCAAGCGCGAGGTGCTCGCCAGCCACGGTGCCCAACCGCGCGCCCTGCG
 CCGCGAGATCGCCGTGACCTGCGTGACGATTGGCCACAAGCCTTGCGGGACAGTGGTTTCGATGCGGCTGCACCGT
 CGGCATGGATTGCCGAAGGGCT

(SEQ ID NO. 715)

Clone X0017

.....X0017SP6.seq:.....
 TTGGGC-TTGGCC-CAATA-GGCCCAATCAAAAGCCGAGCAGGTGGAACCTA-CGCATTGCGCTC-TCGT-
 TGTGCACCCGAGCCATCGCACGCGCGGAATTCCCGGAT-TC-
 CCGTATTCTCCGGCGGCCGGGCTAACCCATCCCA-GCCGAACGGTTGGCTC-
 TGCCGTGGGTCCCGTGTGGCCGATCGGGGCGTCACCGGGGTGCTCGGGTGCGG-TGACCATGGC-AACTGCCCC-
 ATGGGCCGACCCTGTTGTCAGATAAACCTG

(SEQ ID NO. 716)

.....X0017T7.seq:.....

TGGTGGAGGTCCCCACCAA-ACCGGCCGTAACCTCTGCTCACGGAAATGCGG-
 CAGGCCGCGCTAGCACGTGGTATCCGCCATAAAGGTGCACCTTAAGCACGGCGTCCCAATTCTCGAACGACATCTT
 GTGGAAGGTGCCGTGCGCGCAAGATCCCGCGGTGCTCACCACACCGTGACGGCGCCGAATTCGTCAAGCGCGGTCT
 TGATGATGTTGCTGCGCGCTCCTCGGTGGCGACGCTGTCGGTA-
 TTGGCGACCGCCCGCCCCCTTGTCGCGAAATCTCGGCGACGACCTCATCGGCCATCGCCGAACCGGGCGCCCCG

(SEQ ID NO. 717)

Clone X0018

.....X0018SP6.seq:.....
 GCCGGCCAAACTGGCCGGCGGGTTGCTGTC-TCAAGGTGGGTTCGCCACCAA-ACC-
 CACTCAAGGATCGCAAGGAAAGC-
 TCAAGGATGCGGTGCGCGGCCCAAGGCCGCGGTCAAGGAGGGCATCGTCCCTGGTGGGGGA-
 CCTCCCTCATCCACCAGGCCCCGAAGGCGCTGACCGAACTGC-TGCGTC-C-GACCGGTGACAA-
 GTCCCTCGGTGTCCACGTGT-CTCCGAAGCCCTTGCCGCTCCGTTGTTCTGGATC-CC-CCAAC-
 CTGGCTTGGACGGCTC-GTGGTGGTCAACAAGGTACGCGAGCTACCCGCGGGCATGGGCTGAACGTGA

(SEQ ID NO. 718)

Clone X0018

.....X0018T7.seq:.....
 CGAACCT-AATTGTCCTGTAATGCCAGCTACCAA-
 GCATGGCTGGTGGCCGGGGCGGTGAAGCCGGCGTCTGCGGCACCGTCCAATC-ATGTGGAT-
 GCCGGAATGGGATGTCCGG-ACGGCGAATCCGTA-
 TTCGTTGTCCCGTGAGGCCAGGTGGATGGGGGAAGGATC-TGGTGTCCGGGATGAT-
 ATGGGGCCGATGCCGCGGTTGAAGTCCACTGGATCGGGAATTCGGGAATCGTGAT-CCGACGTTACGGCCGAAC

(SEQ ID NO. 719)

Clone X0019

: : : : : X0019SP6.seq: : : : : :

CTAACGGAATGAAAGCCCTGGTGGCCGT-

TCGGCGGTGGCCGTCGTCGCACTGCTCGGTGTATCTTCCGCCCAAGCTGATCCCAGGCGGATCCCAGGCGCAGGTGA

GGCCAACTATGGTGGCCCCCAAGTCCCCACGCTTGTGCGATCACACCGAATGGGCGCA-

TGGGGAATTCTGCCCAGCCTCCGGGTCTACCCGTCCCAAGTTGGGCGTACA-

CCTCCCGCCGCTCGGGATGGCCGCTGCCGACCCGGCCTGGGCC-

AGGTTCTCGCGCTGTACCCGGAAGCCGACACTGCCGGC (SEQ ID NO. 720)

: : : : : X0019T7.seq: : : : : :

CCGCGGGACAC-CCTC-

ATGTCGCCCCATGGACGCGGTGGAACGCAAGCAGCTGATCGAGCTACAACGCCGCGCGGAACGCTTCCGCCGCGGG

CGTGACCGCATCCCGTTGACCGGGCGGATCGCGGTGATCGTCGATGACGGCATCGCCACCGGAGCGACGGCCAAGGC

GGCGTGCCAGGTGCCCCGGGCGCACGGTGCGGACAAGGTGGTGTGGCGGTCCCGATCGGCCCCA-

ACGACATCGTGGCGAAGATTGCGCGGGTACGCCGATGATGTGGTGTGTTGGCGACGCCGCGTTGT

(SEQ ID NO. 721)

Clone X0020

: : : : : X0020T7.seq: : : : : :

CTCTGGGACCGGCCACGGTGCC-

CCGGCGTTCCCGGACGTGCTGCGCCAGGTGTCCGGCGGCCGCGTGCATGGTGTTCGCGATCGGCCGCTGGCCAGAG

CCCACCGGTGAATCTGGCGCCTGGCCGACCACCGTGCGCCGTAGGCTTGCATCGTGCAGCGCTGGCGTGGCCAGGA

CGAGATCCCGACGGATTGGGGCAGATGCGTGCTCACCATCGGGGTATTGACGGCGTGCACCGCGGGCACGCCGAAC

TGATCGCGCACCGGTCAAAGGCGGC (SEQ ID NO. 722)

Clone X0021

: : : : : X0021SP6.seq: : : : : :

AATACTCAAGCTTTCGTCACTTCATTGCGCCAGCAGACCAACAA-AGCATCGGGACATACGGA-

TCAACTACCCGGCCAACGGTGATTTCTTGGCCGCCGCTGACGGCGCGAACGACGCCAGCGACCAC-

TTCAGCAAATGGCCA-CGCGTGCCGGGCCACGAGGTTGGTGTCTCGGCGGCTACTCCCAGGGTGCGGCCGTGATC-

ACATC-TCACCGCCGACCACTGCCCCGGCCTCGGGTTCACGCAGCCGTGCGGCCCGCAGCGAC-

ATCACATCGCCGCGATCGCCCTGTTGCGGAATCCCTC-GGCCGCGCTGGCGGGCTGATTAAC

(SEQ ID NO. 723)

: : : : : X0021T7.seq: : : : : :

TGCCGCGGATTTGGCTGGCTGCCCAATATTAGAATCGGGCCTTTCTTTTTCGCGACAATAAGGTCACAGTAAACC

CTCGTTTTGTGAGATCGGGGCGGGCCGGGCGAA-

TCGACCTCGAGTGAATGGATCTCGAGTGAATGGACAGGGCATCGCCTACGAGTCGCATCCCCATCCAACAGACCGGT

GCTCTTGATCGGACCTGAAGGTCCCGCACGGAGGGTGTGGTTGCCGGCGGGGTACGGTGCGGTAGCGACGTA

GTGTTTGAACGAATTTCTTGATGCTCCAACCTGTTTGGTGTTCATCCAGTTCT

(SEQ ID NO. 724)

Clone X0175

.....X0175SP6.....

AA-CTTGCGCGCTCGGCCGGGTC-AGCATCCAGCTGCTCGGCAAGGAGGCCAGCTAC-C-

TCGCTGCGTATGCCAGCGGTGAGATCCGCCGGGTC-

ACGTCCGCTGCCGCGCACCCTCGGCGAAGTGGGCAATGCCGAGCAGGCAAACATCAACTGGGGCAAGGCCGGTCCG

ATGCGGTGGAAGGGCAAGCGCCCTCGGTCCGGGGCGTGGTGAT-AAACCGGTC-

ACCACCCGCACGGCGGTGGTGAGGGTAAACCTCCGGCGGCCGTACCCGGTTAGCCCGTGGGGCAA

(SEQ ID NO. 725)

.....X0175T7.....

A-TCGAAAGTGACCATCTCTACCTTGAGTGCCATACCGCCGACCCTATGCCTCGGATAGCTCGGCGGAAAGAAACG

CTTGCAAGTGCCGCCGAATAGGCGGTACGTCGTGAGCGCCCATCAACTCTCGCGCGGAGTGATCGCCAGCTGGGCG

GCGCCGACGTGACCGTGGGATTCCGGTGCGCGCCGCGGCCAACGCCCCGATCGTCGACCCGCACGGCAGATCGGC

CGGATGTTCTGAACGCTGCATAGGCACTCCCGCGCGCTGGCAGGCCAGTGCGAACGCCGCGCGGTGCGTCCG

(SEQ ID NO. 726)

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CLAIMS

1. A method for isolating a polynucleotide of interest that is present in a genome of a first mycobacterium strain or that is expressed by said first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain that is different from the first mycobacterium strain or that is not expressed in the second mycobacterium strain, said method comprising:

5 a) contacting under hybridizing conditions the genomic DNA of the first mycobacterium strain with the DNA of at least one clone that belongs to a bacterial artificial chromosome (BAC) genomic DNA library of the second mycobacterium strain ; and

b) isolating the polynucleotide of interest that fails to form a hybrid with the DNA of the second mycobacterium strain.

2. The method according to claim 1, wherein the BAC-based DNA library
15 has been constructed from genomic DNA of *Mycobacterium tuberculosis*.

3. The method according to claim 2, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium tuberculosis* strain H37Rv.

4. The method according to claim 3, wherein the BAC-based DNA library
20 has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on November 19, 1997 under the accession number I-1945.

5. The method according to claim 1, wherein the BAC-based DNA library has been constructed from genomic DNA of *Mycobacterium bovis*.

6. The method according to claim 5, wherein the BAC-based DNA library
25 has been constructed from the genomic DNA of *Mycobacterium bovis* BCG strain Pasteur.

7. The method according to claim 6, wherein the at least one BAC-based DNA library has been deposited in the Collection Nationale de Cultures de Microorganismes (CNCM) on XX XX, 1998 under the accession number I-
30 XXXX.

8. A method of isolating a polynucleotide of interest that is present in a genome of a first mycobacterium strain or that is expressed by the first mycobacterium strain and that is absent or altered in a genome of a second mycobacterium strain or that is not expressed by the second mycobacterium strain, said method comprising :
35

- a) providing at least one polynucleotide contained in a clone of a bacterial artificial chromosome (BAC) DNA library of the first mycobacterium strain;
b) providing at least one genomic or cDNA polynucleotide from a second mycobacterium strain that is different from the first mycobacterium strain or at least one polynucleotide contained in a clone of a BAC DNA library prepared from the genome of the second mycobacterium strain;
c) contacting under hybridizing conditions the polynucleotide of step a) with the polynucleotide of step b); and
d) isolating the polynucleotide of step a) that has not formed a hybrid complex with the polynucleotide of step b).

9. The method of claim 8, wherein the polynucleotide contained in a clone of a BAC DNA library of the first or second mycobacterium strain is prepared by the following procedure :

- 1) digesting at least one recombinant BAC clone by an appropriate restriction endonuclease to yield a polynucleotide insert of interest; and
2) isolating the polynucleotide insert of interest.

10. A purified polynucleotide of interest that has been isolated according to the method of claim 8.

11. The purified polynucleotide of claim 10 which contains at least one Open Reading Frame (ORF).

12. The purified polynucleotide of claim 11, which is SEQ ID N0:1.

13. The purified polynucleotide of claim 11, wherein said polynucleotide is selected from the group consisting of :

- a) a polynucleotide comprising at least 8 consecutive nucleotides of SEQ ID N0:1 ;
b) a polynucleotide having a sequence fully complementary to SEQ ID N0:1 ; and
c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

14. The purified polynucleotide of claim 13, which is SEQ ID N0:2.

15. The purified polynucleotide of claim 13, which is SEQ ID N0:3.

16. The purified polynucleotide of claim 11, wherein the ORF encodes all or part of a polypeptide involved in the pathogenicity of a mycobacterium strain.

17. The purified polynucleotide of claim 11, wherein the ORF encodes all or part of a Polymorphism Glycine Rich Sequence (PGRS).

18. The purified polynucleotide of claim 17, which is SEQ ID N0:4.

19. The purified polynucleotide of claim 17, which is selected from the group consisting of :

a) a polynucleotide comprising at least 8 consecutive nucleotides the of SEQ ID N0:5 ;

b) a polynucleotide having a sequence that is fully complementary to SEQ ID N0:5 ;

c) a polynucleotide that hybridizes under stringent hybridization conditions with the polynucleotide defined in a) or with the polynucleotide defined in b).

20. A pair of the purified polynucleotides as claimed in claim 10.

21. A *Mycobacterium tuberculosis* strain Rv37 genomic DNA library that has been deposited in the Collection Nationale de Cultures de Microorganismes under accession number I-1945, wherein said genomic DNA library comprises recombinant bacterial artificial chromosome vectors.

22. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claim 21.

23. The recombinant BAC vector of claim 22, which is selected from the group consisting of :

Rv101; Rv102; Rv103; Rv104; Rv105; Rv106; Rv107; Rv108; Rv109; Rv10;
Rv110; Rv111; Rv112; Rv113; Rv114; Rv115; Rv116; Rv117; Rv118; Rv119;
Rv11; Rv120; Rv121; Rv122; Rv123; Rv124; Rv126; Rv127; Rv128; Rv129;
Rv130; Rv132; Rv134; Rv135; Rv136; Rv137; Rv138; Rv139; Rv13; Rv140;
Rv141; Rv142; Rv143; Rv144; Rv145; Rv146; Rv147; Rv148; Rv149; Rv14;
Rv150; Rv151; Rv152; Rv153; Rv154; Rv155; Rv156; Rv157; Rv159; Rv15;
Rv160; Rv161; Rv162; Rv163; Rv164; Rv165; Rv166; Rv167; Rv169; Rv16;
Rv170; Rv171; Rv172; Rv173; Rv174; Rv175; Rv176; Rv177; Rv178; Rv179;
Rv17; Rv180; Rv181; Rv182; Rv183; Rv184; Rv185; Rv186; Rv187; Rv188;
Rv18; Rv190; Rv191; Rv192; Rv193; Rv194; Rv195; Rv196; Rv19; Rv1; Rv201;
Rv204; Rv205; Rv207; Rv209; Rv20; Rv214; Rv215; Rv217; Rv218; Rv219;
Rv21; Rv220; Rv221; Rv222; Rv223; Rv224; Rv225; Rv226; Rv227; Rv228;
Rv229; Rv22; Rv230; Rv231; Rv232; Rv233; Rv234; Rv235; Rv237; Rv240;
Rv241; Rv243; Rv244; Rv245; Rv246; Rv247; Rv249; Rv24; Rv251; Rv252;
Rv253; Rv254; Rv255; Rv257; Rv258; Rv259; Rv25; Rv260; Rv261; Rv262;
Rv263; Rv264; Rv265; Rv266; Rv267; Rv268; Rv269; Rv26; Rv270; Rv271;
Rv272; Rv273; Rv274; Rv275; Rv276; Rv277; Rv278; Rv279; Rv27; Rv280;

Rv281; Rv282; Rv283; Rv284; Rv285; Rv286; Rv287; Rv288; Rv289; Rv28;
 Rv290; Rv291; Rv292; Rv293; Rv294; Rv295; Rv296; Rv29; Rv2; Rv301;
 Rv302; Rv303; Rv304; Rv306; Rv307; Rv308; Rv309; Rv30; Rv310; Rv311;
 Rv312; Rv313; Rv314; Rv315; Rv316; Rv317; Rv318; Rv319; Rv31; Rv32;
 5 Rv322; Rv327; Rv328; Rv329; Rv32; Rv330; Rv331; Rv333; Rv334; Rv335;
 Rv336; Rv337; Rv338; Rv339; Rv33; Rv340; Rv341; Rv343; Rv344; Rv346;
 Rv347; Rv348; Rv349; Rv34; Rv350; Rv351; Rv352; Rv353; Rv354; Rv355;
 Rv356; Rv357; Rv358; Rv359; Rv35; Rv360; Rv361; Rv363; Rv364; Rv365;
 Rv366; Rv367; Rv368; Rv369; Rv36; Rv370; Rv371; Rv373; Rv374; Rv375;
 10 Rv376; Rv377; Rv378; Rv379; Rv37; Rv381; Rv382; Rv383; Rv384; Rv385;
 Rv386; Rv387; Rv388; Rv389; Rv38; Rv390; Rv391; Rv392; Rv393; Rv396;
 Rv39; Rv3; Rv40; Rv412; Rv413; Rv414; Rv415; Rv416; Rv417; Rv418; Rv419;
 Rv41; Rv42; Rv43; Rv44; Rv45; Rv46; Rv47; Rv48; Rv49; Rv4; Rv50; Rv51;
 Rv52; Rv53; Rv54; Rv55; Rv56; Rv57; Rv58; Rv59; Rv5; Rv60; Rv61; Rv62;
 15 Rv63; Rv64; Rv65; Rv66; Rv67; Rv68; Rv69; Rv6; Rv70; Rv71; Rv72; Rv73;
 Rv74; Rv75; Rv76; Rv77; Rv78; Rv79; Rv7; Rv80; Rv81; Rv82; Rv83; Rv84;
 Rv85; Rv86; Rv87; Rv88; Rv89; Rv8; Rv90; Rv91; Rv92; Rv94; Rv95; Rv96
 and Rv9.

24. The recombinant BAC vector of claim 22, which is selected from the
 20 group consisting of :
 Rv234; Rv351; Rv166; Rv35; Rv415; Rv404; Rv209; Rv272; Rv30; Rv228;
 Rv233; Rb38; Rv280; Rv177; Rv48; Rv374; Rv151; Rv238; Rv156; Rv92; Rv3;
 Rv403; Rv322; Rv243; Rv330; Rv285; Rv233; Rv219; Rv416; Rv67; Rv222;
 Rv149; Rv279; Rv87; Rv273; Rv266; Rv25; Rv136; Rv414; Rv13; Rv289; Rv60;
 25 Rv104; Rv5; Rv165; Rv215; Rv329; Rv240; Rv19; Rv74; Rv411; Rv167; Rv56;
 Rv80; Rv164; Rv59; Rv313; Rv265; Rv308; Rv220; Rv258; Rv339; Rv121;
 Rv419; Rv418; Rv45; Rv217; Rv134; Rv17; Rv103; Rv21; Rv22; Rv2; Rv270;
 Rv267; Rv174; Rv257; Rv44; Rv71; Rv7; Rv27; Rv191; Rv230; Rv128; Rv407;
 Rv106; Rv39; Rv255; Rv74; Rv355; Rv268; Rv58; Rv173; Rv264; Rv417;
 30 Rv401; Rv144; Rv302; Rv81; Rv163; Rv281; Rv221; Rv420; Rv175; Rv86;
 Rv412; Rv73; Rv269; Rv214; Rv287; Rv42 and Rv143.

25. A *Mycobacterium bovis* BCG strain Pasteur genomic DNA library,
 wherein said genomic DNA library comprises recombinant bacterial artificial
 chromosome vectors.

26. A recombinant bacterial artificial chromosome (BAC) vector, which belongs to the genomic DNA library of claim 25.

27. A recombinant BAC vector according to claim 26, which is selected from the group consisting of :

5 X0001; X0002; X0003; X0004; X0006; X0007; X0008; X0009; X0010; X0012; X0013; X0014; X0015; X0016; X0017; X0018; X0019; X0020; X0021 and X0175.

28. A method for detecting a mycobacterial nucleic acid in a biological sample comprising the steps of :

10 a) contacting the recombinant BAC vector according to claim 22 or 26, or a purified polynucleotide according to claim 10 with the mycobacterial nucleic acid in the biological sample ; and

b) detecting a hybrid nucleic acid molecule formed between said recombinant BAC vector or said purified polynucleotide and the mycobacterial nucleic acid in
15 the biological sample.

29. The method of claim 28, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

30. A method for detecting mycobacterial nucleic acid in a biological sample comprising the steps of :

20 a) contacting a first polynucleotide according to claim 10 that has been immobilized onto a substrate with the mycobacterial nucleic acid in the biological sample ; and

b) contacting a hybrid nucleic acid molecule formed between said first polynucleotide and the mycobacterial nucleic acid in the biological sample with a
25 second, labeled polynucleotide according to claim 10, wherein said second polynucleotide and said first polynucleotide have non-overlapping sequences.

31. The method of claim 30, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization
30 reaction.

32. The method of claim 30 or 31, further comprising before step b), removing the mycobacterial nucleic acid that is not hybridized with the immobilized first polynucleotide.

33. A method for detecting mycobacterial nucleic acid in a biological sample comprising the steps of :

- a) contacting the mycobacterial nucleic acid in the biological sample with a pair of purified polynucleotides according to claim 20 ;
- b) amplifying said mycobacterial nucleic acid ; and
- c) detecting the amplified mycobacterial nucleic acid.

5 34. The method of claim 33, further comprising before step a), making the mycobacterial nucleic acid in the biological sample available to a hybridization reaction.

 35. A kit for detecting a mycobacterium in a biological sample comprising :

- 10 a) a recombinant BAC vector according to claim 22 or 26, or a purified polynucleotide according to claim 10 ; and
- b) reagents necessary to perform a nucleic acid hybridization reaction.

 36. A kit for detecting a mycobacterium in a biological sample comprising :

- 15 a) a recombinant BAC vector according to claim 22 or 26, or a first polynucleotide according to claim 10 that is immobilized onto a substrate ;
- b) reagents necessary to perform a nucleic acid hybridization reaction ; and
- c) a second polynucleotide according to claim 10, wherein said second polynucleotide is radioactively or non-radioactively labeled, and wherein said
- 20 second polynucleotide and said first polynucleotide have non-overlapping sequences.

 37. A kit for detecting a mycobacterium in a biological sample comprising :

- a) a pair of purified polynucleotides according to claim 20 ; and
- 25 b) reagents necessary to perform a nucleic acid amplification reaction.

 38. A method for detecting the presence of a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising the steps of :

- a) contacting the biological sample with a plurality of BAC vectors according to claim 22 or 26, or purified polynucleotides according to claim 10 that are
- 30 immobilized on a substrate ; and
- b) detecting the hybrid complexes formed.

 39. A kit for detecting a genomic DNA, a cDNA or a mRNA of a mycobacterium in a biological sample, comprising :

- a) a substrate on which a plurality of BAC vectors according to claim 22 or 26, or
- 35 purified polynucleotides according to claim 10 have been immobilized.

40. A method for detecting a polynucleotide of mycobacterial origin in a biological sample, said method comprising :

a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 on the surface of a substrate ;

5 b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned ; and

c) detecting a hybrid nucleic acid molecule formed between the polynucleotide in the biological sample and the aligned polynucleotide of step a).

41. A kit for detecting a polynucleotide of mycobacterial origin in a
10 biological sample, comprising :

a) a substrate on which at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 has been aligned.

42. The method of claim 9, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further
15 comprises amplifying the polynucleotide insert.

43. The method of claim 9, wherein the procedure by which the polynucleotide contained in a clone of a BAC DNA library is prepared, further comprises digesting the polynucleotide insert with at least one restriction endonuclease.

20 44. The method of claim 42, further comprising digesting the amplified polynucleotide insert with at least one restriction endonuclease.

45. The Polynucleotide of claim 16, wherein the mycobacterium strain is *Mycobacterium tuberculosis*.

46. The method of claim 33, wherein the amplified mycobacterial DNA is
25 detected by gel electrophoresis or with a labeled polynucleotide according to claim 10.

47. The kit of claim 37, further comprising a polynucleotide according to claim 10.

48. The kit of claim 39, further comprising reagents necessary to perform a
30 hybridization reaction.

49. A method for physically mapping a polynucleotide of mycobacterial origin in a biological sample, said method comprising:

a) aligning at least one polynucleotide contained in a recombinant BAC vector according to claim 22 or 26 on the surface of a substrate;

- b) contacting the polynucleotide in the biological sample with the substrate on which the polynucleotide of step a) has been aligned under hybridizing conditions; and
 - c) detecting the location of the hybridized polynucleotide from the biological sample.
- 5

50. The kit of claim 41, further comprising reagents necessary for labeling DNA and reagents necessary for performing a hybridization reaction.